



SEQUENCE LISTING

<110> SERVANT, GUY
OZECK, MARK
BRUST, PAUL
XU, HONG

<120> FUNCTIONAL COUPLING OF T1RS AND T2RS BY GI PROTEINS
AND CELL-BASED ASSAYS FOR THE IDENTIFICATION OF T1R
AND T2R MODULATORS

<130> 100337.54281US

<140> 10/770,127

<141> 2004-02-03

<150> 60/444,172

<151> 2003-02-03

<150> 60/457,318

<151> 2003-03-26

<160> 210

<170> PatentIn version 3.2

<210> 1

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<212> PRT

<213> Homo sapiens

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Ile	Asp	Leu	Ile	Lys	His	Arg	Lys	Met	Ala	Pro	Leu	Asp	Leu	Leu	Leu
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Ser	Cys	Leu	Ala	Val	Ser	Arg	Ile	Phe	Leu	Gln	Leu	Phe	Ile	Phe	Tyr
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Val	Asn	Val	Ile	Val	Ile	Phe	Phe	Ile	Glu	Phe	Ile	Met	Cys	Ser	Ala
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Asn	Cys	Ala	Ile	Leu	Leu	Phe	Ile	Asn	Glu	Leu	Glu	Leu	Trp	Leu	Ala
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Thr	Trp	Leu	Gly	Val	Phe	Tyr	Cys	Ala	Lys	Val	Ala	Ser	Val	Arg	His
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Pro	Leu	Phe	Ile	Trp	Leu	Lys	Met	Arg	Ile	Ser	Lys	Leu	Val	Pro	Trp
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 Phe Ser Phe Val Ala Glu Phe Ser Val Pro Leu Leu Ile Phe Leu Phe
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 Ala Val Leu Leu Leu Ile Phe Ser Leu Gly Arg His Thr Arg Gln Met
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 Arg Asn Thr Val Ala Gly Ser Arg Val Pro Gly Arg Gly Ala Pro Ile
 210 215 220
 Ser Ala Leu Leu Ser Ile Leu Ser Phe Leu Ile Leu Tyr Phe Ser His
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 245 250 255
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Cys Asn Glu Leu Ile Lys His Arg Lys Leu Met Pro Ile Gln Ile Leu
35        40        45

Leu Met Cys Ile Gly Met Ser Arg Phe Gly Leu Gln Met Val Leu Met
50        55        60

Val Gln Ser Phe Phe Ser Val Phe Phe Pro Leu Leu Tyr Val Lys Ile
65        70        75        80

Ile Tyr Gly Ala Ala Met Met Phe Leu Trp Met Phe Phe Ser Ser Ile
85        90        95

Ser Leu Trp Phe Ala Thr Cys Leu Ser Val Phe Tyr Cys Leu Lys Ile
100       105       110

Ser Gly Phe Thr Gln Ser Cys Phe Leu Trp Leu Lys Phe Arg Ile Pro
115       120       125

Lys Leu Ile Pro Trp Leu Phe Trp Glu Ala Phe Trp Pro Leu Ala Leu
130       135       140

His Leu Cys Val Glu Val Asp Tyr Ala Lys Asn Val Glu Glu Asp Ala
145       150       155       160

Leu Arg Asn Thr Thr Leu Lys Lys Ser Lys Thr Lys Ile Lys Lys Ile
165       170       175

Ser Glu Val Leu Leu Val Asn Leu Ala Leu Ile Phe Pro Leu Ala Ile
180       185       190

Phe Val Met Cys Thr Ser Met Leu Leu Ile Ser Leu Tyr Lys His Thr
195       200       205

His Arg Met Gln His Gly Ser His Gly Phe Arg Asn Ala Asn Thr Glu
210       215       220

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 245 250 255
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Thr	Thr	Leu	Ala	Leu	Leu	Arg	Ile	Ile	Leu	Leu	Cys	Ile	Ile	Leu	Thr
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65					70					75				80	
Ile	Met	Gln	Ile	Ile	Asp	Val	Ser	Trp	Thr	Phe	Thr	Asn	His	Leu	Ser
			85						90					95	
Ile	Trp	Leu	Ala	Thr	Cys	Leu	Gly	Val	Leu	Tyr	Cys	Leu	Lys	Ile	Ala
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Thr	Ala	Ser	Leu	Ile	Asn	Glu	Phe	Lys	Leu	Tyr	Ser	Val	Phe	Arg	Gly
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His Leu Lys Pro Gly Ser Lys Gly Pro Ile Phe Ser
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Ser	Ala	Phe	Phe	Val	Leu	Cys	Phe	Met	Phe	Leu	Asp	Ser	Ser	Ser	Val	85	90	95
Trp	Phe	Val	Thr	Leu	Leu	Asn	Ile	Leu	Tyr	Cys	Val	Lys	Ile	Thr	Asn	100	105	110
Phe	Gln	His	Ser	Val	Phe	Leu	Leu	Leu	Lys	Arg	Asn	Ile	Ser	Pro	Lys	115	120	125
Ile	Pro	Arg	Leu	Leu	Leu	Ala	Cys	Val	Leu	Ile	Ser	Ala	Phe	Thr	Thr	130	135	140
Cys	Leu	Tyr	Ile	Thr	Leu	Ser	Gln	Ala	Ser	Pro	Phe	Pro	Glu	Leu	Val	145	150	155
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Leu	Val	Val	Ser	Leu	Val	Leu	Ser	Ser	Ser	Leu	Gln	Phe	Ile	Ile	Asn	180	185	190
Val	Thr	Ser	Ala	Ser	Leu	Leu	Ile	His	Ser	Leu	Arg	Arg	His	Ile	Gln	195	200	205
Lys	Met	Gln	Lys	Asn	Ala	Thr	Gly	Phe	Trp	Asn	Pro	Gln	Thr	Glu	Ala	210	215	220
His	Val	Gly	Ala	Met	Lys	Leu	Met	Val	Tyr	Phe	Leu	Ile	Leu	Tyr	Ile	225	230	235
Pro	Tyr	Ser	Val	Ala	Thr	Leu	Val	Gln	Tyr	Leu	Pro	Phe	Tyr	Ala	Gly	245	250	255
Met	Asp	Met	Gly	Thr	Lys	Ser	Ile	Cys	Leu	Ile	Phe	Ala	Thr	Leu	Tyr	260	265	270
Ser	Pro	Gly	His	Ser	Val	Leu	Ile	Ile	Ile	Thr	His	Pro	Lys	Leu	Lys	275	280	285
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35        40        45

Leu Gly Leu Ala Gly Cys Arg Phe Leu Leu Gln Trp Leu Ile Ile Leu
50        55        60

Asp Leu Ser Leu Phe Pro Leu Phe Gln Ser Ser Arg Trp Leu Arg Tyr
65        70        75        80

Leu Ser Ile Phe Trp Val Leu Val Ser Gln Ala Ser Leu Trp Phe Ala
85        90        95

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 Gly Leu Thr Phe Tyr His Pro Pro Gln Gly Asn Ser Ser Ile Arg Tyr
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 Pro Phe Glu Ser Trp Gln Tyr Leu Tyr Ala Phe Gln Leu Asn Ser Gly
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 Ser Tyr Leu Pro Leu Val Val Phe Leu Val Ser Ser Gly Met Leu Ile
 180 185 190
 Val Ser Leu Tyr Thr His His Lys Lys Met Lys Val His Ser Ala Gly
 195 200 205
 Arg Arg Asp Val Arg Ala Lys Ala His Ile Thr Ala Leu Lys Ser Leu
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 Gly Cys Phe Leu Leu Leu His Leu Val Tyr Ile Met Ala Ser Pro Phe
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 245 250 255
 Trp Glu Thr Leu Met Ala Ala Tyr Pro Ser Leu His Ser Leu Ile Leu
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Arg Gly Trp Val Lys Lys Met Gly Val Pro Ile Asn Ser His Asp Ser
35          40          45

Gly Lys Pro Leu Ser Pro Thr Gln Ala Asp His Val Gly His Lys Ser
50          55          60

Val Ser Thr Phe Pro Glu Gln Trp Leu Ala Leu Leu Ser Cys Leu Arg
65          70          75          80

Val Leu Val Ser Gln Ala Asn Met Phe Ala Thr Phe Phe Ser Gly Phe
85          90          95

Cys Cys Met Glu Ile Met Thr Phe Val Xaa Xaa Xaa Xaa Xaa Xaa Xaa
100         105         110

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Leu Val
115         120         125

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 Ser Val Pro Leu Val Phe Leu Arg His His Arg Lys Met Glu Asp His
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 Thr Ala Val Arg Arg Arg Leu Lys Pro Arg Xaa Xaa Xaa Xaa Xaa Xaa
 195 200 205
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 Ala Arg His Phe Ser Met Thr Phe Ser Pro Ser Asp Leu Thr Ile Leu
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tcaaaccaag gtgctcatcg ctctgaactt ccccttttac atggtttctg ccttggccag 660
 acacttttcc atgaccttct aatctccctc tgatctcacc attcttgcca tctctgcaac 720
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<210> 13
 <211> 318
 <212> PRT
 <213> Homo sapiens

<400> 13
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 Met Asp Trp Val Lys Lys Arg Lys Ile Ala Ser Ile Asp Leu Ile Leu
 35 40 45
 Thr Ser Leu Ala Ile Ser Arg Ile Cys Leu Leu Cys Val Ile Leu Leu
 50 55 60
 Asp Cys Phe Ile Leu Val Leu Tyr Pro Asp Val Tyr Ala Thr Gly Lys
 65 70 75 80
 Glu Met Arg Ile Ile Asp Phe Phe Trp Thr Leu Thr Asn His Leu Ser
 85 90 95
 Ile Trp Phe Ala Thr Cys Leu Ser Ile Tyr Tyr Phe Phe Lys Ile Gly
 100 105 110
 Asn Phe Phe His Pro Leu Phe Leu Trp Met Lys Trp Arg Ile Asp Arg
 115 120 125
 Val Ile Ser Trp Ile Leu Leu Gly Cys Val Val Leu Ser Val Phe Ile
 130 135 140
 Ser Leu Pro Ala Thr Glu Asn Leu Asn Ala Asp Phe Arg Phe Cys Val
 145 150 155 160
 Lys Ala Lys Arg Lys Thr Asn Leu Thr Trp Ser Cys Arg Val Asn Lys
 165 170 175
 Thr Gln His Ala Ser Thr Lys Leu Phe Leu Asn Leu Ala Thr Leu Leu
 180 185 190
 Pro Phe Cys Val Cys Leu Met Ser Phe Phe Leu Leu Ile Leu Ser Leu
 195 200 205
 Arg Arg His Ile Arg Arg Met Gln Leu Ser Ala Thr Gly Cys Arg Asp
 210 215 220

Pro Ser Thr Glu Ala His Val Arg Ala Leu Lys Ala Val Ile Ser Phe
 225 230 235 240

Leu Leu Leu Phe Ile Ala Tyr Tyr Leu Ser Phe Leu Ile Ala Thr Ser
 245 250 255

Ser Tyr Phe Met Pro Glu Thr Glu Leu Ala Val Ile Phe Gly Glu Ser
 260 265 270

Ile Ala Leu Ile Tyr Pro Ser Ser His Ser Phe Ile Leu Ile Leu Gly
 275 280 285

Asn Asn Lys Leu Arg His Ala Ser Leu Lys Val Ile Trp Lys Val Met
 290 295 300

Ser Ile Leu Lys Gly Arg Lys Phe Gln Gln His Lys Gln Ile
 305 310 315

<210> 14

<211> 957

<212> DNA

<213> Homo sapiens

<400> 14

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attgcctcca ttgatttaat cctcacaagt ctggccatat ccagaatttg tctattgtgc	180
gtaatactat tagattgttt tatattggtg ctatatccag atgtctatgc cactggtaaa	240
gaaatgagaa tcattgactt cttctggaca ctaaccaatc atttaagtat ctggtttgca	300
acctgcctca gcatttacta tttcttcaag ataggttaatt tctttcaccc acttttcctc	360
tggatgaagt ggagaattga caggggtgatt tcctggattc tactgggggtg cgtggttctc	420
tctgtgttta ttagccttcc agccactgag aatttgaacg ctgatttcag gttttgtgtg	480
aaggcaaaga ggaaaacaaa cttaacttgg agttgcagag taaataaaac tcaacatgct	540
tctaccaagt tatcttctcaa cctggcaacg ctgctccctt tttgtgtgtg cctaattgtc	600
tttttcctct tgatcctctc cctgcggaga catatcaggc gaatgcagct cagtgcaca	660
gggtgcagag accccagcac agaagcccat gtgagagccc tgaaagctgt catttccttc	720
cttctcctct ttattgccta ctatttgtcc tttctcattg ccacctccag ctactttatg	780
ccagagacgg aattagctgt gatttttggt gagtccatag ctctaactta cccctcaagt	840
cattcattta tctaatactt gggaacaat aaattaagac atgcatctct aaaggtgatt	900
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<210> 15
 <211> 309
 <212> PRT
 <213> Homo sapiens

<400> 15

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Phe	Ile	Leu	Gly	Ile	Leu	Gly	Asn	Gly	Tyr	Ile	Ala	Leu	Val	Asn	Trp
			20					25					30		
Ile	Asp	Trp	Ile	Lys	Lys	Lys	Lys	Ile	Ser	Thr	Val	Asp	Tyr	Ile	Leu
		35					40					45			
Thr	Asn	Leu	Val	Ile	Ala	Arg	Ile	Cys	Leu	Ile	Ser	Val	Met	Val	Val
	50					55					60				
Asn	Gly	Ile	Val	Ile	Val	Leu	Asn	Pro	Asp	Val	Tyr	Thr	Lys	Asn	Lys
65					70				75					80	
Gln	Gln	Ile	Val	Ile	Phe	Thr	Phe	Trp	Thr	Phe	Ala	Asn	Tyr	Leu	Asn
				85					90					95	
Met	Trp	Ile	Thr	Thr	Cys	Leu	Asn	Val	Phe	Tyr	Phe	Leu	Lys	Ile	Ala
			100					105					110		
Ser	Ser	Ser	His	Pro	Leu	Phe	Leu	Trp	Leu	Lys	Trp	Lys	Ile	Asp	Met
		115					120					125			
Val	Val	His	Trp	Ile	Leu	Leu	Gly	Cys	Phe	Ala	Ile	Ser	Leu	Leu	Val
	130					135					140				
Ser	Leu	Ile	Ala	Ala	Ile	Val	Leu	Ser	Cys	Asp	Tyr	Arg	Phe	His	Ala
145					150					155					160
Ile	Ala	Lys	His	Lys	Arg	Asn	Ile	Thr	Glu	Met	Phe	His	Val	Ser	Lys
				165					170					175	
Ile	Pro	Tyr	Phe	Glu	Pro	Leu	Thr	Leu	Phe	Asn	Leu	Phe	Ala	Ile	Val
			180					185					190		
Pro	Phe	Ile	Val	Ser	Leu	Ile	Ser	Phe	Phe	Leu	Leu	Val	Arg	Ser	Leu
	195						200					205			
Trp	Arg	His	Thr	Lys	Gln	Ile	Lys	Leu	Tyr	Ala	Thr	Gly	Ser	Arg	Asp
	210					215						220			
Pro	Ser	Thr	Glu	Val	His	Val	Arg	Ala	Ile	Lys	Thr	Met	Thr	Ser	Phe
225					230					235					240
Ile	Phe	Phe	Phe	Phe	Leu	Tyr	Tyr	Ile	Ser	Ser	Ile	Leu	Met	Thr	Phe
				245					250					255	
Ser	Tyr	Leu	Met	Thr	Lys	Tyr	Lys	Leu	Ala	Val	Glu	Phe	Gly	Glu	Ile
		260						265					270		

Ala Ala Ile Leu Tyr Pro Leu Gly His Ser Leu Ile Leu Ile Val Leu
 275 280 285

Asn Asn Lys Leu Arg Gln Thr Phe Val Arg Met Leu Thr Cys Arg Lys
 290 295 300

Ile Ala Cys Met Ile
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<210> 16
 <211> 930
 <212> DNA
 <213> Homo sapiens

<400> 16
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 atttccacag ttgactacat ccttaccaat ttagttatcg ccagaatttg tttgatcagt 180
 gtaatgggtg taaatggcat tgtaatagta ctgaaccag atgtttatac aaaaaataaa 240
 caacagatag tcattttttac cttctggaca tttgccaaact acttaaatat gtggattacc 300
 acctgcctta atgtcttcta ttttctgaag atagccagtt cctctcatcc actttttctc 360
 tggctgaagt ggaaaattga tatggtggtg cactggatcc tgctgggatg ctttgccatt 420
 tccttgttgg tcagccttat agcagcaata gtactgagtt gtgattatag gtttcatgca 480
 attgccaaac ataaaagaaa cattactgaa atgttccatg tgagtaaaat accatacttt 540
 gaacccttga ctctctttta cctgtttgca attgtcccat ttattgtgtc actgatatca 600
 tttttccttt tagtaagatc tttatggaga cataccaagc aaataaaaact ctatgctacc 660
 ggcagtagag accccagcac agaagttcat gtgagagcca ttaaaaactat gacttcattt 720
 atcttctttt ttttcctata ctatatttct tctattttga tgacctttag ctatcttatg 780
 aaaaaataca agttagctgt ggagtttggg gagattgcag caattctcta ccccttgggt 840
 cactcactta ttttaattgt tttaaataat aaactgaggc agacatttgt cagaatgctg 900
 acatgtagaa aaattgcctg catgatatga 930

<210> 17
 <211> 312
 <212> PRT
 <213> Homo sapiens

<400> 17
 Met Pro Ser Ala Ile Glu Ala Ile Tyr Ile Ile Leu Ile Ala Gly Glu
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Leu Thr Ile Gly Ile Trp Gly Asn Gly Phe Ile Val Leu Val Asn Cys
 20 25 30
 Ile Asp Trp Leu Lys Arg Arg Asp Ile Ser Leu Ile Asp Ile Ile Leu
 35 40 45
 Ile Ser Leu Ala Ile Ser Arg Ile Cys Leu Leu Cys Val Ile Ser Leu
 50 55 60
 Asp Gly Phe Phe Met Leu Leu Phe Pro Gly Thr Tyr Gly Asn Ser Val
 65 70 75 80
 Leu Val Ser Ile Val Asn Val Val Trp Thr Phe Ala Asn Asn Ser Ser
 85 90 95
 Leu Trp Phe Thr Ser Cys Leu Ser Ile Phe Tyr Leu Leu Lys Ile Ala
 100 105 110
 Asn Ile Ser His Pro Phe Phe Phe Trp Leu Lys Leu Lys Ile Asn Lys
 115 120 125
 Val Met Leu Ala Ile Leu Leu Gly Ser Phe Leu Ile Ser Leu Ile Ile
 130 135 140
 Ser Val Pro Lys Asn Asp Asp Met Trp Tyr His Leu Phe Lys Val Ser
 145 150 155 160
 His Glu Glu Asn Ile Thr Trp Lys Phe Lys Val Ser Lys Ile Pro Gly
 165 170 175
 Thr Phe Lys Gln Leu Thr Leu Asn Leu Gly Val Met Val Pro Phe Ile
 180 185 190
 Leu Cys Leu Ile Ser Phe Phe Leu Leu Leu Phe Ser Leu Val Arg His
 195 200 205
 Thr Lys Gln Ile Arg Leu His Ala Thr Gly Phe Arg Asp Pro Ser Thr
 210 215 220
 Glu Ala His Met Arg Ala Ile Lys Ala Val Ile Ile Phe Leu Leu Leu
 225 230 235 240
 Leu Ile Val Tyr Tyr Pro Val Phe Leu Val Met Thr Ser Ser Ala Leu
 245 250 255
 Ile Pro Gln Gly Lys Leu Val Leu Met Ile Gly Asp Ile Val Thr Val
 260 265 270
 Ile Phe Pro Ser Ser His Ser Phe Ile Leu Ile Met Gly Asn Ser Lys
 275 280 285
 Leu Arg Glu Ala Phe Leu Lys Met Leu Arg Phe Val Lys Cys Phe Leu
 290 295 300
 Arg Arg Arg Lys Pro Phe Val Pro
 305 310

<210> 18
 <211> 939
 <212> DNA
 <213> Homo sapiens

<400> 18
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 atttccttga ttgacatcat cctgatcagc ttggccatct ccagaatctg tctgctgtgt 180
 gtaatatcat tagatggctt ctttatgctg ctctttccag gtacatatgg caatagcgtg 240
 ctagtaagca ttgtgaatgt tgtctggaca tttgccaata attcaagtct ctggtttact 300
 tcttgccctca gtatcttcta tttactcaag atagccaata tatcgacccc atttttcttc 360
 tggctgaagc taaagatcaa caaggatcatg cttgcgattc ttctgggggtc ctttcttatac 420
 tctttaatta ttagtggtcc aaagaatgat gatatgtggt atcacctttt caaagtcagt 480
 catgaagaaa acattacttg gaaattcaaa ctgagtaaaa ttccaggtag tttcaaacag 540
 ttaaccctga acctgggggt gatgggtccc tttatccttt gcctgatctc atttttcttg 600
 ttacttttct ccctagttag acacaccaag cagattcgac tgcattgtac agggttcaga 660
 gaccccgata cagaggccca catgagggcc ataaaggcag tgatcatctt tctgctctc 720
 ctcatcgtgt actaccaggt ctttcttggt atgacctcta gcgctctgat tcctcagggg 780
 aaattagtgt tgatgattgg tgacatagta actgtcattt tcccatcaag ccattcattc 840
 attctaatta tgggaaatag caagttgagg gaagcttttc tgaagatggt aagatttgtg 900
 aagtgtttcc ttagaagaag aaagcctttt gttccatag 939

<210> 19
 <211> 307
 <212> PRT
 <213> Homo sapiens

<400> 19
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 Ser Val Phe Gly Val Leu Gly Asn Gly Phe Ile Gly Leu Val Asn Cys
 20 25 30
 Ile Asp Cys Ala Lys Asn Lys Leu Ser Thr Ile Gly Phe Ile Leu Thr
 35 40 45
 Gly Leu Ala Ile Ser Arg Ile Phe Leu Ile Trp Ile Ile Ile Thr Asp
 50 55 60

Gly Phe Ile Gln Ile Phe Ser Pro Asn Ile Tyr Ala Ser Gly Asn Leu
 65 70 75 80
 Ile Glu Tyr Ile Ser Tyr Phe Trp Val Ile Gly Asn Gln Ser Ser Met
 85 90 95
 Trp Phe Ala Thr Ser Leu Ser Ile Phe Tyr Phe Leu Lys Ile Ala Asn
 100 105 110
 Phe Ser Asn Tyr Ile Phe Leu Trp Leu Lys Ser Arg Thr Asn Met Val
 115 120 125
 Leu Pro Phe Met Ile Val Phe Leu Leu Ile Ser Ser Leu Leu Asn Phe
 130 135 140
 Ala Tyr Ile Ala Lys Ile Leu Asn Asp Tyr Lys Thr Lys Asn Asp Thr
 145 150 155 160
 Val Trp Asp Leu Asn Met Tyr Lys Ser Glu Tyr Phe Ile Lys Gln Ile
 165 170 175
 Leu Leu Asn Leu Gly Val Ile Phe Phe Phe Thr Leu Ser Leu Ile Thr
 180 185 190
 Cys Ile Phe Leu Ile Ile Ser Leu Trp Arg His Asn Arg Gln Met Gln
 195 200 205
 Ser Asn Val Thr Gly Leu Arg Asp Ser Asn Thr Glu Ala His Val Lys
 210 215 220
 Ala Met Lys Val Leu Ile Ser Phe Ile Ile Leu Phe Ile Leu Tyr Phe
 225 230 235 240
 Ile Gly Met Ala Ile Glu Ile Ser Cys Phe Thr Val Arg Glu Asn Lys
 245 250 255
 Leu Leu Leu Met Phe Gly Met Thr Thr Thr Ala Ile Tyr Pro Trp Gly
 260 265 270
 His Ser Phe Ile Leu Ile Leu Gly Asn Ser Lys Leu Lys Gln Ala Ser
 275 280 285
 Leu Arg Val Leu Gln Gln Leu Lys Cys Cys Glu Lys Arg Lys Asn Leu
 290 295 300
 Arg Val Thr
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<210> 20

<211> 924

<212> DNA

<213> Homo sapiens

<400> 20

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tctacgattg gctttattct caccggctta gctatttcaa gaatttttct gatatggata 180
ataattacag atggatttat acagatatcc tctccaaata tatatgcctc cggtaaccta 240
attgaatata ttagttactt ttgggtaatt ggtaatcaat caagtatgtg gtttgccacc 300
agcctcagca tcttctattt cctgaagata gcaaattttt ccaactacat atttctctgg 360
ttgaagagca gaacaaatat ggttcttccc ttcattgatag tattcttact tatttcacg 420
ttacttaatt ttgcatacat tgcgaagatt cttaatgatt ataaaacgaa gaatgacaca 480
gtctgggatc tcaacatgta taaaagtga tactttatta aacagatttt gctaaatctg 540
ggagtcattt tcttctttac actatcccta attacatgta tttttttaat catttcctt 600
tgagagacaca acaggcagat gcaatcgaat gtgacaggat tgagagactc caacacagaa 660
gctcatgtga aggcaatgaa agttttgata tctttcatca tcctctttat cttgtatttt 720
ataggcatgg ccatagaaat atcatgtttt actgtgagag aaaacaaact gctgcttatg 780
tttggaatga caaccacagc catctatccc tggggtcact catttatctt aattctagga 840
aacagcaagc taaagcaagc ctctttgagg gtactgcagc aattgaagtg ctgtgagaaa 900
aggaaaaatc tcagagtcac atag 924

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<210> 21
<211> 242
<212> PRT
<213> Homo sapiens

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<220>
<221> MOD_RES
<222> (58)..(89)
<223> Variable amino acid

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Phe Ile Met Gly Ile Gln Arg Ser Arg Val Met Val Leu Val His Cys
20          25          30
Ile Asp Trp Ile Arg Arg Trp Lys Leu Ser Leu Ile Asp Phe Ile Leu
35          40          45
Thr Cys Trp Ala Ile Ser Arg Ile Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa
50          55          60
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
65          70          75          80
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn His Leu Cys Thr Phe Ala
85          90          95

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Thr Cys Leu Ala Val Phe Tyr Phe Leu Lys Ile Val Asn Phe Ser Tyr
 100 105 110
 Leu Phe Tyr Phe Trp Leu Lys Trp Arg Ile Asn Lys Val Ala Phe Ile
 115 120 125
 Leu Pro Leu Val Ser Ala Phe Ser Val Tyr Gln Leu Ser Phe Asp Val
 130 135 140
 His Phe Cys Leu Leu Val Ser Cys Pro Lys Lys Tyr Glu Arg His Met
 145 150 155 160
 Thr Gly Leu Leu Asn Val Ser Asn Asn Lys Asn Val Asn Asn Ile Ile
 165 170 175
 Ile Phe Phe Ile Gly Ser Leu Ser Ser Phe Ser Ile Ser Ser Ile Phe
 180 185 190
 Phe Leu Leu Leu Leu Leu Ser Ser Arg His Met Lys His Ile Arg Phe
 195 200 205
 Asn Phe Arg Asp Cys Arg Thr Pro Val Tyr Gly Pro Ile Ser Glu Pro
 210 215 220
 Arg Lys Arg Phe Ser Phe Phe Val Leu Leu Leu Tyr Lys Asn Leu Pro
 225 230 235 240

Phe Ser

<210> 22
 <211> 309
 <212> PRT
 <213> Homo sapiens

<400> 22
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 Ile Met Gly Thr Val Gly Asn Phe Ile Val Leu Val Asn Ile Ile Asp
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 Ile Arg Asn Lys Val Ser Leu Ile Asp Phe Ile Leu Asn Cys Leu Ala
 35 40 45
 Ile Ser Arg Ile Cys Phe Leu Ile Thr Ile Leu Ala Thr Ser Phe Asn
 50 55 60
 Ile Gly Tyr Glu Lys Met Pro Asp Ser Lys Asn Leu Ala Val Ser Phe
 65 70 75 80
 Asp Ile Leu Trp Thr Gly Ser Ser Tyr Phe Cys Leu Ser Cys Thr Thr
 85 90 95
 Cys Leu Ser Val Phe Tyr Phe Leu Lys Val Ala Asn Phe Ser Asn Pro
 100 105 110

Ile Phe Leu Trp Met Lys Trp Lys Ile His Lys Val Leu Leu Phe Ile
 115 120 125
 Val Leu Glu Ala Thr Ile Ser Phe Cys Thr Thr Ser Ile Leu Lys Glu
 130 135 140
 Ile Ile Ile Asn Ser Leu Ile Glu Arg Val Thr Ile Lys Gly Asn Leu
 145 150 155 160
 Thr Phe Asn Tyr Met Asp Thr Met His Asp Phe Thr Ser Leu Phe Leu
 165 170 175
 Leu Gln Met Met Phe Ile Leu Pro Phe Val Glu Thr Leu Ala Ser Ile
 180 185 190
 Leu Leu Leu Ile Leu Ser Leu Trp Ser His Thr Arg Gln Met Lys Leu
 195 200 205
 His Gly Ile Tyr Ser Arg Asp Pro Ser Thr Glu Ala His Val Lys Pro
 210 215 220
 Ile Lys Ala Ile Ile Ser Phe Leu Leu Leu Phe Ile Val His Tyr Phe
 225 230 235 240
 Ile Ser Ile Ile Leu Thr Leu Ala Cys Pro Leu Leu Asp Phe Val Ala
 245 250 255
 Ala Arg Thr Phe Ser Ser Val Leu Val Phe Phe His Pro Ser Gly His
 260 265 270
 Ser Phe Leu Leu Ile Leu Arg Asp Ser Lys Leu Lys Gln Ala Ser Leu
 275 280 285
 Cys Val Leu Lys Lys Met Lys Tyr Ala Lys Lys Asp Ile Ile Ser His
 290 295 300
 Phe Tyr Lys His Ala
 305

<210> 23

<211> 948

<212> DNA

<213> Homo sapiens

<400> 23

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 gtctccctga ttgattttat tctcaactgc ttggccatct ccaggatatg tttcctgtag 180
 ataacaattt tagctacctc tttcaatata ggctatgaga aaatgcctga ttctaagaat 240
 cttgcagtaa gttttgacat tctctggaca ggatccagct atttctgcct gtcctgtacc 300
 acttgcctca gtgtcttcta tttcctcaag gtagccaact tctccaatcc cattttcctc 360

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tggatgaaat ggaaaattca caaggtgctt ctctttattg tactagaggc aacgatctct 420
ttctgcacaa cttccattct gaaggaaata ataattaata gtttaattcta agaacgggta 480
acaataaaaag gcaacttgac atttaattat atggatacca tgcattgattt cacttctctg 540
tttctccttc agatgatggt catccttctt tttgtggaaa cactggcttc cattcttctc 600
ttaatcctct ccttatggag ccacaccagg cagatgaagc tacatgggtat ttattccagg 660
gatcccagca cagaagccca tgtaaaacct ataaaagcta taatttcatt tctactctc 720
tttattgtgc attatttcat cagtatcata ctaacattgg cctgtcctct tctagacttc 780
gttgcggaag ggacttttag tagtgtgtg gtatttttcc atccatctgg ccattcattt 840
cttctaattt tacgggacag caaactgaag caagcttctc tctgtgtcct gaagaagatg 900
aagtatgcca aaaaggacat aatctctcat tttataaac atgcctga 948

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<210> 24

<211> 303

<212> PRT

<213> Homo sapiens

<400> 24

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Met Glu Ser Ala Leu Pro Ser Ile Phe Thr Leu Val Ile Ile Ala Glu
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Phe Ile Ile Gly Asn Leu Ser Asn Gly Phe Ile Val Leu Ile Asn Cys
20           25           30

Ile Asp Trp Val Ser Lys Arg Glu Leu Ser Ser Val Asp Lys Leu Leu
35           40           45

Ile Ile Leu Ala Ile Ser Arg Ile Gly Leu Ile Trp Glu Ile Leu Val
50           55           60

Ser Trp Phe Leu Ala Leu His Tyr Leu Ala Ile Phe Val Ser Gly Thr
65           70           75           80

Gly Leu Arg Ile Met Ile Phe Ser Trp Ile Val Ser Asn His Phe Asn
85           90           95

Leu Trp Leu Ala Thr Ile Phe Ser Ile Phe Tyr Leu Leu Lys Ile Ala
100          105          110

Ser Phe Ser Ser Pro Ala Phe Leu Tyr Leu Lys Trp Arg Val Asn Lys
115          120          125

Val Ile Leu Met Ile Leu Leu Gly Thr Leu Val Phe Leu Phe Leu Asn
130          135          140

Leu Ile Gln Ile Asn Met His Ile Lys Asp Trp Leu Asp Arg Tyr Glu
145          150          155          160

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Arg	Asn	Thr	Thr	Trp	Asn	Phe	Ser	Met	Ser	Asp	Phe	Glu	Thr	Phe	Ser
				165					170					175	
Val	Ser	Val	Lys	Phe	Thr	Met	Thr	Met	Phe	Ser	Leu	Thr	Pro	Phe	Thr
			180					185					190		
Val	Ala	Phe	Ile	Ser	Phe	Leu	Leu	Leu	Ile	Phe	Ser	Leu	Gln	Lys	His
		195					200					205			
Leu	Gln	Lys	Met	Gln	Leu	Asn	Tyr	Lys	Gly	His	Arg	Asp	Pro	Arg	Thr
	210					215					220				
Lys	Val	His	Thr	Asn	Ala	Leu	Lys	Ile	Val	Ile	Ser	Phe	Leu	Leu	Phe
225					230					235					240
Tyr	Ala	Ser	Phe	Phe	Leu	Cys	Val	Leu	Ile	Ser	Trp	Ile	Ser	Glu	Leu
				245					250					255	
Tyr	Gln	Asn	Thr	Val	Ile	Tyr	Met	Leu	Cys	Glu	Thr	Ile	Gly	Val	Phe
			260					265					270		
Ser	Pro	Ser	Ser	His	Ser	Phe	Leu	Leu	Ile	Leu	Gly	Asn	Ala	Lys	Leu
		275					280					285			
Arg	Gln	Ala	Phe	Leu	Leu	Val	Ala	Ala	Lys	Val	Trp	Ala	Lys	Arg	
	290					295					300				

<210> 25

<211> 912

<212> DNA

<213> Homo sapiens

<400> 25

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ctgtcctcag tcgataaact cctcattatc ttggcaatct ccagaattgg gctgatctgg	180
gaaatattag taagttgggt tttagctctg cattatctag ccatatttgt gtctggaaca	240
ggattaagaa ttatgatttt tagctggata gtttctaadc acttcaatct ctggcttgct	300
acaatcttca gcatctttta tttgctcaaa atagcgagtt tctctagccc tgcttttctc	360
tatttgaagt ggagagtaaa caaagtgatt ctgatgatac tgctaggaac cttgggtcttc	420
ttatttttaa atctgatata aataaacatg catataaaag actggctgga ccgatatgaa	480
agaaacacaa cttggaattt cagtatgagt gactttgaaa cattttcagt gtcgggtcaaa	540
ttcactatga ctatgttcag tctaacacca tttactgtgg ccttcatctc ttttctcctg	600
ttaattttct ccctgcagaa acatctccag aaaatgcaac tcaattacaa aggacacaga	660
gacccagga ccaaggtcca tacaaatgcc ttgaaaattg tgatctcatt ctttttattc	720

tatgctagtt tctttctatg tgttctcata tcatggattt ctgagctgta tcagaacaca 780
 gtgatctaca tgctttgtga gacgattgga gtcttctctc cttcaagcca ctcctttctt 840
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<210> 26
 <211> 317
 <212> PRT
 <213> Homo sapiens

<400> 26
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 Ile Asp Trp Val Lys Gly Arg Lys Ile Ser Ser Val Asp Arg Ile Leu
 35 40 45
 Thr Ala Leu Ala Ile Ser Arg Ile Ser Leu Val Trp Leu Ile Phe Gly
 50 55 60
 Ser Trp Cys Val Ser Val Phe Phe Pro Ala Leu Phe Ala Thr Glu Lys
 65 70 75 80
 Met Phe Arg Met Leu Thr Asn Ile Trp Thr Val Ile Asn His Phe Ser
 85 90 95
 Val Trp Leu Ala Thr Gly Leu Gly Thr Phe Tyr Phe Leu Lys Ile Ala
 100 105 110
 Asn Phe Ser Asn Ser Ile Phe Leu Tyr Leu Lys Trp Arg Val Lys Lys
 115 120 125
 Val Val Leu Val Leu Leu Leu Val Thr Ser Val Phe Leu Phe Leu Asn
 130 135 140
 Ile Ala Leu Ile Asn Ile His Ile Asn Ala Ser Ile Asn Gly Tyr Arg
 145 150 155 160
 Arg Asn Lys Thr Cys Ser Ser Asp Ser Ser Asn Phe Thr Arg Phe Ser
 165 170 175
 Ser Leu Ile Val Leu Thr Ser Thr Val Phe Ile Phe Ile Pro Phe Thr
 180 185 190
 Leu Ser Leu Ala Met Phe Leu Leu Leu Ile Phe Ser Met Trp Lys His
 195 200 205
 Arg Lys Lys Met Gln His Thr Val Lys Ile Ser Gly Asp Ala Ser Thr
 210 215 220

Lys Ala His Arg Gly Val Lys Ser Val Ile Thr Phe Phe Leu Leu Tyr
 225 230 235 240
 Ala Ile Phe Ser Leu Ser Phe Phe Ile Ser Val Trp Thr Ser Glu Arg
 245 250 255
 Leu Glu Glu Asn Leu Ile Ile Leu Ser Gln Val Met Gly Met Ala Tyr
 260 265 270
 Pro Ser Cys His Ser Cys Val Leu Ile Leu Gly Asn Lys Lys Leu Arg
 275 280 285
 Gln Ala Ser Leu Ser Val Leu Leu Trp Leu Arg Tyr Met Phe Lys Asp
 290 295 300
 Gly Glu Pro Ser Gly His Lys Glu Phe Arg Glu Ser Ser
 305 310 315

<210> 27

<211> 954

<212> DNA

<213> Homo sapiens

<400> 27

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atctcttcgg ttgatcggat cctcactgct ttggcaatct ctggaattag cctgggttgg	180
ttaatattcg gaagctggtg tgtgtctgtg tttttccag ctttatttgc cactgaaaaa	240
atgttcagaa tgcttactaa tatctggaca gtgatcaatc atttttagtgt ctgggttagct	300
acaggcctcg gtacttttta ttttctcaag atagccaatt tttctaactc tatttttctc	360
tacctaaagt ggagggttaa aaagggtggt ttggtgctgc ttcttgtgac ttcggtcttc	420
ttgtttttta atattgcact gataaacatc catataaatg ccagtatcaa tggatacaga	480
agaaacaaga cttgcagttc tgattcaagt aactttacac gattttccag tcttattgta	540
ttaaccagca ctgtgttcat tttcataccc tttactttgt ccctggcaat gtttcttctc	600
ctcatcttct ccatgtggaa acatcgcaag aagatgcagc aactgtcaa aatatccgga	660
gacgccagca ccaaagccca cagaggagt aaaagtgtga tcaactttctt cctactctat	720
gccattttct ctctgtcttt tttcatatca gtttggacct ctgaaagggt ggaggaaaat	780
ctaattattc tttcccaggt gatgggaatg gcttatcctt catgtcactc atgtgttctg	840
attcttggaa acaagaagct gagacaggcc tctctgtcag tgctactgtg gctgaggtag	900
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<210> 28
 <211> 299
 <212> PRT
 <213> Homo sapiens

<400> 28

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			20					25					30		
Ile	Glu	Trp	Val	Lys	Arg	Gln	Lys	Ile	Ser	Phe	Ala	Asp	Gln	Ile	Leu
		35					40					45			
Thr	Ala	Leu	Ala	Val	Ser	Arg	Val	Gly	Leu	Leu	Trp	Val	Ile	Leu	Leu
	50					55					60				
His	Trp	Tyr	Ala	Thr	Val	Leu	Asn	Pro	Gly	Ser	Tyr	Ser	Leu	Gly	Val
65					70					75				80	
Arg	Ile	Thr	Thr	Ile	Asn	Ala	Trp	Ala	Val	Thr	Asn	His	Phe	Ser	Ile
				85					90					95	
Trp	Val	Ala	Thr	Ser	Leu	Ser	Ile	Phe	Tyr	Phe	Leu	Lys	Ile	Ala	Asn
			100					105					110		
Phe	Ser	Asn	Phe	Ile	Phe	Leu	His	Leu	Lys	Arg	Arg	Ile	Lys	Ser	Val
		115					120					125			
Ile	Pro	Val	Ile	Leu	Leu	Gly	Ser	Leu	Leu	Phe	Leu	Val	Cys	His	Leu
	130					135					140				
Val	Val	Val	Asn	Met	Asp	Glu	Ser	Met	Trp	Thr	Lys	Glu	Tyr	Glu	Gly
145					150					155					160
Asn	Val	Ser	Trp	Glu	Ile	Lys	Leu	Ser	Asp	Pro	Thr	His	Leu	Ser	Asp
				165					170					175	
Met	Thr	Val	Thr	Thr	Leu	Ala	Asn	Leu	Ile	Pro	Phe	Thr	Leu	Ser	Leu
			180					185					190		
Leu	Ser	Phe	Leu	Leu	Leu	Ile	Cys	Ser	Leu	Cys	Lys	His	Leu	Lys	Lys
		195					200					205			
Met	Gln	Phe	His	Gly	Lys	Gly	Ser	Pro	Asp	Ser	Asn	Thr	Lys	Val	His
	210					215					220				
Ile	Lys	Ala	Leu	Gln	Thr	Val	Thr	Ser	Phe	Leu	Leu	Leu	Phe	Ala	Val
225					230					235				240	
Tyr	Phe	Leu	Ser	Leu	Ile	Thr	Ser	Ile	Trp	Asn	Phe	Arg	Arg	Arg	Leu
				245					250					255	
Asn	Glu	Pro	Val	Leu	Met	Leu	Ser	Gln	Thr	Thr	Ala	Ile	Ile	Tyr	Pro
			260					265					270		

Ser Phe His Ser Phe Ile Leu Ile Trp Gly Ser Lys Lys Leu Lys Gln
 275 280 285

Thr Phe Leu Leu Ile Leu Cys Gln Ile Lys Cys
 290 295

<210> 29
 <211> 903
 <212> DNA
 <213> Homo sapiens

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 atctcctttg ctgaccaa atctcactgct ctggcagtct ccagagttgg tttgctctgg 180
 gtaatattat tacattggta tgcaactggt ttgaatccag gttcatatag tttaggagta 240
 agaattacta ctattaatgc ctgggctgta accaaccatt tcagcatctg ggttgctact 300
 agcctcagca tattttatatt cctcaagatt gccaatctct ccaactttat ttttcttcac 360
 ttaaaaagga gaattaagag tgtcattcca gtgatactat tggggctctt gttatTTTTg 420
 gtttgtcatc ttgttgtggt aaacatggat gagagtatgt ggacaaaaga atatgaagga 480
 aacgtgagtt gggagatcaa attgagtgat cgcacgcacc tttcagatat gactgtaacc 540
 acgcttgcaa acttaatacc ctttactctg tcctgttat cttttctgct cttaatctgt 600
 tctttgtgta aacatctcaa gaagatgcag ttccatggca aaggatctcc agattccaac 660
 accaaggtcc acataaaagc ttgcaaacg gtgacctcct tctcttgtt atttgcgtgt 720
 tactttctgt ccctaatac atcgatttg aatttttagga ggaggctgta gaacgaacct 780
 gtccatcatgc tcagccaaac tactgcaatt atataccctt catttcattc attcatccta 840
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 tga 903

<210> 30
 <211> 291
 <212> PRT
 <213> Homo sapiens

<400> 30
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Glu Ser Leu Thr Ile Ile Val Gln Ser Ser Leu Ile Val Ala Val Leu
 20 25 30

Gly	Arg	Glu	Trp	Leu	Gln	Val	Arg	Arg	Leu	Met	Pro	Val	Asp	Met	Ile
		35					40					45			
Leu	Ile	Ser	Leu	Gly	Ile	Ser	Arg	Phe	Cys	Leu	Gln	Trp	Ala	Ser	Met
	50					55					60				
Leu	Asn	Asn	Phe	Cys	Ser	Tyr	Phe	Asn	Leu	Asn	Tyr	Val	Leu	Cys	Asn
65					70					75					80
Leu	Thr	Ile	Thr	Trp	Glu	Phe	Phe	Asn	Ile	Leu	Thr	Phe	Trp	Leu	Asn
				85					90					95	
Ser	Leu	Leu	Thr	Val	Phe	Tyr	Cys	Ile	Lys	Val	Ser	Ser	Phe	Thr	His
			100					105					110		
His	Ile	Phe	Leu	Trp	Leu	Arg	Trp	Arg	Ile	Leu	Arg	Leu	Phe	Pro	Trp
		115					120					125			
Ile	Leu	Leu	Gly	Ser	Leu	Met	Ile	Thr	Cys	Val	Thr	Ile	Ile	Pro	Ser
	130					135					140				
Ala	Ile	Gly	Asn	Tyr	Ile	Gln	Ile	Gln	Leu	Leu	Thr	Met	Glu	His	Leu
145					150					155					160
Pro	Arg	Asn	Ser	Thr	Val	Thr	Asp	Lys	Leu	Glu	Asn	Phe	His	Gln	Tyr
				165					170					175	
Gln	Phe	Gln	Ala	His	Thr	Val	Ala	Leu	Val	Ile	Pro	Phe	Ile	Leu	Phe
			180					185					190		
Leu	Ala	Ser	Thr	Ile	Phe	Leu	Met	Ala	Ser	Leu	Thr	Lys	Gln	Ile	Gln
		195					200					205			
His	His	Ser	Thr	Gly	His	Cys	Asn	Pro	Ser	Met	Lys	Ala	Arg	Phe	Thr
	210					215					220				
Ala	Leu	Arg	Ser	Leu	Ala	Val	Leu	Phe	Ile	Val	Phe	Thr	Ser	Tyr	Phe
225					230					235					240
Leu	Thr	Ile	Leu	Ile	Thr	Ile	Ile	Gly	Thr	Leu	Phe	Asp	Lys	Arg	Cys
				245					250					255	
Trp	Leu	Trp	Val	Trp	Glu	Ala	Phe	Val	Tyr	Ala	Phe	Ile	Leu	Met	His
			260					265					270		
Ser	Thr	Ser	Leu	Met	Leu	Ser	Ser	Pro	Thr	Leu	Lys	Arg	Ile	Leu	Lys
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Gly	Lys	Cys													
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<210> 31

<211> 876

<212> DNA

<213> Homo sapiens


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<400> 31
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aggctgatgc ctgtggacat gattctcatc agcctgggca tctctcgctt ctgtctacag      180
tgggcatcaa tgctgaacaa tttttgctcc tattttaatt tgaattatgt actttgcaac      240
ttaacaatca cctgggaatt ttttaatatc cttacattct ggttaaacag cttgcttacc      300
gtgttctact gcatcaaggc ctcttctttc acccatcaca tctttctctg gctgaggtgg      360
agaattttga ggttggttcc ctggatatta ctgggttctc tgatgattac ttgtgtaaca      420
atcatccctt cagctattgg gaattacatt caaattcagt tactcaccat ggagcatcta      480
ccaagaaaca gcaactgaac tgacaaactt gaaaattttc atcagtatca gttccaggct      540
catacagttg cattgggtat tcttttcatc ctgttcctgg cctccaccat ctttctcatg      600
gcatcactga ccaagcagat acaacatcat agcactggtc actgcaatcc aagcatgaaa      660
gcgcgcttca ctgccctgag gtcccttgcc gtcttattta ttgtgtttac ctcttacttt      720
ctaaccatac tcatcaccat tataggtact ctatttgata agagatgttg gttatgggtc      780
tggaagctt ttgtctatgc ttcatctta atgcattcca cttcactgat gctgagcagc      840
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<210> 32
<211> 330
<212> PRT
<213> Homo sapiens

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<220>
<221> MOD_RES
<222> (5)..(5)
<223> Variable amino acid

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<220>
<221> MOD_RES
<222> (61)..(61)
<223> Variable amino acid

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<220>
<221> MOD_RES
<222> (207)..(207)
<223> Variable amino acid

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<400> 32
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Ala Phe Val Leu Gly Asn Val Ala Asn Gly Phe Ile Ala Leu Ile Asn
20           25           30

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Val	Asn	Asp	Trp	Val	Lys	Thr	Gln	Lys	Ile	Ser	Ser	Thr	Asp	Gln	Ile	35	40	45
Val	Thr	Ala	Leu	Ala	Phe	Ser	Arg	Ile	Gly	Leu	Leu	Xaa	Thr	Leu	Ile	50	55	60
Ile	Leu	Leu	His	Trp	Tyr	Ala	Thr	Val	Phe	Asn	Ser	Ala	Leu	Tyr	Ser	65	70	75
Leu	Glu	Val	Arg	Ile	Val	Pro'	Ser	Asn	Val	Ser	Ala	Ile	Ile	Asn	His	85	90	95
Phe	Ser	Ile	Trp	Leu	Ala	Thr	Ser	Leu	Ser	Ile	Phe	Tyr	Leu	Phe	Lys	100	105	110
Ile	Ala	Asn	Phe	Ser	Asn	Phe	Ile	Phe	Leu	His	Leu	Lys	Lys	Arg	Ile	115	120	125
Lys	Ser	Val	Leu	Leu	Val	Ile	Leu	Leu	Gly	Ser	Leu	Val	Phe	Leu	Ile	130	135	140
Cys	Asn	Leu	Ala	Val	Val	Thr	Met	Asp	Asp	Ser	Val	Trp	Thr	Lys	Glu	145	150	155
Phe	Glu	Gly	Asn	Val	Thr	Trp	Lys	Ile	Glu	Leu	Arg	Asn	Ala	Ile	His	165	170	175
Leu	Ser	Asn	Met	Thr	Ile	Thr	Asn	His	Ala	Ser	Lys	Leu	His	Thr	Val	180	185	190
His	Ser	Asp	Ser	Asn	Ile	Phe	Ser	Ala	Val	Ser	Leu	Phe	Ser	Xaa	Thr	195	200	205
Met	Leu	Ala	Asn	Phe	Thr	Leu	Phe	Ile	Leu	Thr	Leu	Ile	Ser	Phe	Leu	210	215	220
Leu	Leu	Val	Cys	Ser	Pro	Cys	Lys	His	Leu	Lys	Met	Met	Gln	Leu	His	225	230	235
Gly	Lys	Gly	Ser	Gln	Asp	Leu	Ser	Thr	Lys	Val	His	Ile	Lys	Pro	Leu	245	250	255
Gln	Thr	Val	Ile	Ser	Phe	Arg	Met	Leu	Phe	Ala	Ile	Tyr	Phe	Leu	Cys	260	265	270
Ile	Ile	Thr	Ser	Thr	Trp	Asn	Pro	Arg	Thr	Gln	Gln	Ser	Asn	Leu	Val	275	280	285
Phe	Leu	Leu	Tyr	Gln	Thr	Leu	Ala	Ile	Met	Tyr	Pro	Ser	Phe	His	Ser	290	295	300
Phe	Ile	Leu	Ile	Met	Arg	Ser	Arg	Lys	Leu	Lys	Gln	Thr	Ser	Leu	Ser	305	310	315
Val	Leu	Cys	Gln	Val	Thr	Cys	Trp	Val	Lys							325	330	

<210> 33
 <211> 313
 <212> PRT
 <213> Homo sapiens

<400> 33

Met	Phe	Val	Gly	Ile	Asn	Ile	Phe	Phe	Leu	Val	Val	Ala	Thr	Arg	Gly	1	5	10	15
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Ile	Glu	Trp	Ala	Lys	Ser	Trp	Lys	Val	Ser	Ser	Ala	Asp	Phe	Ile	Leu	35	40	45	
Thr	Ser	Leu	Ala	Ile	Val	Arg	Ile	Ile	Arg	Leu	Tyr	Leu	Ile	Leu	Phe	50	55	60	
Asp	Ser	Phe	Ile	Met	Val	Leu	Ser	Pro	His	Leu	Tyr	Thr	Ile	Arg	Lys	65	70	75	80
Leu	Val	Lys	Leu	Phe	Thr	Ile	Leu	Trp	Ala	Leu	Ile	Asn	Gln	Leu	Ser	85	90	95	
Ile	Phe	Ala	Thr	Cys	Leu	Ser	Ile	Phe	Tyr	Leu	Leu	Lys	Ile	Ala	Asn	100	105	110	
Phe	Ser	His	Ser	Leu	Phe	Leu	Trp	Leu	Lys	Trp	Arg	Met	Asn	Gly	Met	115	120	125	
Ile	Val	Met	Leu	Leu	Ile	Leu	Ser	Leu	Phe	Leu	Leu	Ile	Phe	Asp	Ser	130	135	140	
Leu	Val	Leu	Glu	Ile	Phe	Ile	Asp	Ile	Ser	Leu	Asn	Ile	Ile	Asp	Lys	145	150	155	160
Ser	Asn	Leu	Thr	Leu	Tyr	Leu	Asp	Glu	Ser	Lys	Thr	Leu	Tyr	Asp	Lys	165	170	175	
Leu	Ser	Ile	Leu	Lys	Thr	Leu	Leu	Ser	Leu	Thr	Tyr	Val	Ile	Pro	Phe	180	185	190	
Leu	Leu	Thr	Leu	Thr	Ser	Leu	Leu	Leu	Phe	Ile	Ser	Leu	Val	Arg	195	200	205		
His	Thr	Lys	Asn	Leu	Gln	Leu	Asn	Ser	Leu	Gly	Ser	Arg	Asp	Ser	Ser	210	215	220	
Thr	Glu	Ala	His	Lys	Arg	Ala	Met	Lys	Met	Val	Ile	Ala	Phe	Leu	Leu	225	230	235	240
Leu	Phe	Ile	Ile	Asn	Phe	Ile	Ser	Thr	Leu	Ile	Gly	Asp	Trp	Ile	Phe	245	250	255	
Leu	Glu	Val	Glu	Asn	Tyr	Gln	Val	Met	Met	Phe	Ile	Met	Met	Ile	Leu	260	265	270	

Leu Ala Phe Pro Ser Gly His Ser Phe Ile Ile Ile Leu Gly Asn Asn
 275 280 285

Lys Leu Arg Gln Ser Ser Leu Arg Leu Leu Trp His Leu Lys Phe Ser
 290 295 300

Leu Lys Lys Ala Lys Pro Leu Thr Ser
 305 310

<210> 34

<211> 945

<212> DNA

<213> Homo sapiens

<400> 34

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gtctcatcag ctgatttcat cctcaccagc ttggctatag tcagaatcat tcgactgtat      180
ttaatactat ttgattcatt tataatggta ttgtcccctc atctatatac catccgtaaa      240
ctagtaaaac tgtttactat tctttgggca ttaattaatc agttaagtat ctagtttgcc      300
acctgcctaa gcattttcta cttgcttaag atagccaatt tctcccactc ccttttcttc      360
tggctgaagt ggagaatgaa cggaatgatt gttatgcttc ttatatgtgc tttgttctta      420
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aaaagtaatc tgactttata tttagatgaa agtaaaactc tctatgataa actctctatt      540
ttaaaaaactc ttctcagctt gacatacggt attcccttctc ttctgactct gacctctttg      600
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tcaagggact ccagcacaga ggcccataaa agggccatga aaatggatgat agccttcctc      720
ctccttttta ttattaactt tatttccact ttaataggag attggatctt ccttgaggta      780
gagaattatc aggtcatgat gtttattatg atgattttac ttgcctttcc ctcaggccac      840
tcatttatta taattttggg aaacaacaag ctaagacaga gctccttgag actactgtgg      900
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<210> 35

<211> 121

<212> PRT

<213> Homo sapiens

<400> 35

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 Leu His Ser Lys Gly Ser Gln Asp Pro Ser Thr Lys Val His Ile Lys
 35 40 45
 Ala Leu Gln Thr Val Thr Ser Phe Leu Met Leu Phe Ala Ile Tyr Phe
 50 55 60
 Leu Cys Ile Ile Thr Ser Thr Trp Asn Leu Arg Thr Gln Gln Ser Lys
 65 70 75 80
 Leu Val Leu Leu Leu Cys Gln Thr Val Ala Ile Met Tyr Pro Ser Phe
 85 90 95
 His Ser Phe Ile Leu Ile Met Gly Ser Arg Lys Leu Lys Gln Thr Phe
 100 105 110
 Leu Ser Val Leu Trp Gln Met Thr Cys
 115 120

<210> 36
 <211> 466
 <212> DNA
 <213> Homo sapiens

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 atcccagcac caaggtccat ataaaagctt tgcaaactgt gacctccttc ctcatgttat 180
 ttgccattta ctttctgtgt ataatcacat caacttgga tcttaggaca cagcagagca 240
 aacttggtact cctgctttgc caaactgttg caatcatgta tccttcattc cactcattca 300
 tcctgattat gggagtagg aagctaaaac agacctttct ttcagttttg tggcagatga 360
 catgctgagt gaaagaagag aaaccctcaa ctccatagat tcacaagggg agcatcgtgg 420
 gtcttctagc agaaaacaaa ctgatgggtgt ctggaacatt ttatat 466

<210> 37
 <211> 129
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (3)..(3)
 <223> Variable amino acid

<400> 37
 His Leu Xaa Arg Lys Ala Lys Ser Val Val Leu Val Ile Val Leu Gly
 1 5 10 15

Ser Leu Phe Phe Leu Val Cys Gln Leu Val Met Lys Asn Thr Tyr Ile
 20 25 30
 Asn Val Trp Thr Glu Glu Cys Glu Gly Asn Val Thr Trp Lys Ile Lys
 35 40 45
 Leu Arg Asn Ala Met His Leu Ser Asn Leu Thr Val Ala Met Leu Ala
 50 55 60
 Asn Leu Ile Pro Phe Thr Leu Thr Val Ile Ser Phe Leu Leu Leu Ile
 65 70 75 80
 Tyr Ser Leu Cys Lys His Leu Lys Lys Met Gln Leu His Gly Lys Gly
 85 90 95
 Ser Gln Asp Pro Ser Thr Lys Ile His Ile Lys Ala Leu Gln Thr Val
 100 105 110
 Thr Ser Phe Leu Val Leu Leu Ala Ile Tyr Phe Leu Cys Leu Ile Ile
 115 120 125

Ser

<210> 38
 <211> 397
 <212> DNA
 <213> Homo sapiens

 <220>
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 <222> (12)..(12)
 <223> n is a, c, g, or t

<400> 38
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 tctttttggt ttgtcaactt gtgatgaaaa acacgtatat aaatgtgttg acagaagaat 120
 gtgaaggaaa cgtaacttgg aagatcaaac tgaggaatgc aatgcacctt tccaacttga 180
 ctgtagccat gctagcaaac ttgataccat tcaactctgac cgtgatatct tttctgctgt 240
 taatctactc tctgtgtaaa catctgaaga agatgcagct ccatggcaaa ggatctcaag 300
 atcccagcac caagatccac ataaaagctc tgcaaactgt gacctccttc ctcgattac 360
 ttgccattta ctttctgtgt ctaatcatat ccttttg 397

<210> 39
 <211> 299
 <212> PRT
 <213> Homo sapiens

<400> 39

Met Pro Pro Gly Ile Gly Asn Thr Phe Leu Ile Val Met Met Gly Glu
 1 5 10 15
 Phe Ile Ile Met Leu Gly Asn Gly Phe Ile Val Leu Val Asn Cys Ile
 20 25 30
 Asp Trp Gly Val Lys Ser Tyr Thr Thr Ala Ser Ser Pro Ala Trp Leu
 35 40 45
 Ser Pro Gln Ser Val Asn Phe Gly Tyr Tyr Leu Ile His Leu Gln His
 50 55 60
 Tyr Gly His Ile Tyr Met Pro Ser Ile Asn Asn Leu Phe Ile Phe Phe
 65 70 75 80
 Gly His Pro Ile Thr Leu Pro Gly Leu Leu Pro Cys Phe Leu Leu Leu
 85 90 95
 Asn Thr Tyr Phe Ser His Pro Cys Phe Ile Trp Leu Arg Trp Arg Ile
 100 105 110
 Ser Arg Thr Leu Leu Glu Leu Pro Leu Gly Ser Leu Leu Leu Leu Phe
 115 120 125
 Phe Asn Leu Ala Leu Thr Gly Gly Leu Ser Asp Leu Trp Ile Asn Ile
 130 135 140
 Tyr Thr Ile Tyr Glu Arg Asn Ser Thr Trp Ser Leu Asp Val Ser Lys
 145 150 155 160
 Ile Leu Tyr Cys Ser Leu Trp Ile Leu Val Ser Leu Ile Tyr Leu Ile
 165 170 175
 Ser Phe Leu Leu Ser Leu Ile Ser Leu Leu Leu Leu Ile Leu Ser Leu
 180 185 190
 Met Arg His Ile Arg Asn Leu Gln Leu Asn Thr Met Gly Pro Arg Asp
 195 200 205
 Leu Arg Met Lys Ala His Lys Arg Ala Met Lys Met Lys Met Lys Met
 210 215 220
 Met Val Ser Phe Leu Leu Phe Phe Leu Val His Phe Ser Ser Leu Leu
 225 230 235 240
 Pro Thr Gly Trp Ile Phe Leu Ile Gln Gln Lys Gln Ala Asn Phe Phe
 245 250 255
 Val Leu Leu Thr Ser Ile Ile Phe Pro Ser Ser His Ser Phe Val Leu
 260 265 270
 Ile Leu Glu Asn Cys Lys Leu Arg Gln Thr Ala Val Gly Pro Leu Trp
 275 280 285
 His Leu Lys Cys His Leu Lys Arg Val Lys Leu
 290 295

<210> 40
 <211> 90
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (35)..(35)
 <223> Variable amino acid

<220>
 <221> MOD_RES
 <222> (39)..(39)
 <223> Variable amino acid

<220>
 <221> MOD_RES
 <222> (82)..(82)
 <223> Variable amino acid

<400> 40
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 1 5 10 15
 Phe Ile Ile Ser Met Leu Gly Asn Val Phe Ile Gly Leu Val Asn Cys
 20 25 30
 Ser Glu Xaa Ile Lys Asn Xaa Lys Val Phe Ser Ala Asp Phe Ile Leu
 35 40 45
 Thr Cys Leu Ala Ile Ser His Asn Gly Gln Leu Leu Val Ile Leu Phe
 50 55 60
 Asp Ser Phe Leu Val Gly Leu Ala Ser His Leu Tyr Thr Thr Tyr Arg
 65 70 75 80
 Leu Xaa Lys Asn Cys Ile Met Leu Trp Thr
 85 90

<210> 41
 <211> 656
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (10)..(10)
 <223> n is a, c, g, or t

<220>
 <221> modified_base
 <222> (68)..(68)
 <223> n is a, c, g, or t

<220>
 <221> modified_base
 <222> (82)..(82)
 <223> n is a, c, g, or t

<220>
 <221> modified_base
 <222> (112)..(112)
 <223> n is a, c, g, or t

<220>
 <221> modified_base
 <222> (125)..(125)
 <223> n is a, c, g, or t

<220>
 <221> modified_base
 <222> (187)..(187)
 <223> n is a, c, g, or t

<220>
 <221> modified_base
 <222> (242)..(242)
 <223> n is a, c, g, or t

<220>
 <221> modified_base
 <222> (260)..(260)
 <223> n is a, c, g, or t

<220>
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 <222> (282)..(282)
 <223> n is a, c, g, or t

<220>
 <221> modified_base
 <222> (397)..(397)
 <223> n is a, c, g, or t

<220>
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 <222> (411)..(411)
 <223> n is a, c, g, or t

<220>
 <221> modified_base
 <222> (538)..(538)
 <223> n is a, c, g, or t

<220>
 <221> modified_base
 <222> (629)..(629)
 <223> n is a, c, g, or t

<400> 41
 tatagggaacn gtgatgcttc gtacactctc caagaagaaa cactccgtga ggtatgtgag 60

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actgcatncc ttagtagatc tnttgggata tatattcata atatagaaaa anaggcaaag 120
acttnccttaa gtatatgaga ctctatccaa cagcagaagg ttctgatcaa gactggaagt 180
gcaatanaag caatgaagat aagtatcaga tatgaatgct cttctgcaat ggtctgattg 240
tnacattatt aatgatacan agtattaaaa acttggattt tnttgtctct ggagatggcc 300
accgaatcgg acacaaatct tctgattctg gcaatagcag aattcatcat cagcatgctg 360
gggaatgtgt tcattggact ggtaaactgc tctgaangga tcaagaacca naaggtcttc 420
tcagctgact tcatcctcac ctgcttggct atctctcaca atggacaact gttggtgata 480
ctgtttgatt catttctagt gggacttgct tcacatctat ataccacata tagactanga 540
aaaaactgta ttatgctttg gacatgacta atcacttgac aactgcttc gcacgtgcta 600
gcatattcta ttcttagata gccacttcnc actccttgct tctgctgaag tgggat 656

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<210> 42
<211> 70
<212> PRT
<213> Homo sapiens

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<220>
<221> MOD_RES
<222> (21)..(21)
<223> Variable amino acid

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<220>
<221> MOD_RES
<222> (44)..(44)
<223> Variable amino acid

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<220>
<221> MOD_RES
<222> (47)..(47)
<223> Variable amino acid

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<220>
<221> MOD_RES
<222> (62)..(62)
<223> Variable amino acid

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<400> 42
Val Ala Phe Val Leu Gly Asn Val Ala Asn Gly Phe Ile Ala Leu Val
1           5           10           15

Asn Val Ile Asp Xaa Val Asn Thr Arg Lys Ile Ser Ser Ala Glu Gln
          20           25           30

Ile Leu Thr Ala Leu Val Val Ser Arg Ile Gly Xaa Thr Leu Xaa His
35           40           45

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Ser Ile Pro Asp Ala Thr Arg Cys Ser Ala Leu Tyr Arg Xaa Glu Val
 50 55 60

Arg Ile Val Ala Ser Asn
 65 70

<210> 43
 <211> 589
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> modified_base
 <222> (39)..(39)
 <223> n is a, c, g, or t

<220>
 <221> modified_base
 <222> (42)..(42)
 <223> n is a, c, g, or t

<220>
 <221> modified_base
 <222> (321)..(321)
 <223> n is a, c, g, or t

<220>
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 <222> (375)..(375)
 <223> n is a, c, g, or t

<220>
 <221> modified_base
 <222> (414)..(414)
 <223> n is a, c, g, or t

<220>
 <221> modified_base
 <222> (481)..(482)
 <223> n is a, c, g, or t

<220>
 <221> modified_base
 <222> (490)..(490)
 <223> n is a, c, g, or t

<220>
 <221> modified_base
 <222> (541)..(541)
 <223> n is a, c, g, or t

<400> 43
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 gagaatgtat atgaagagga gtgaatttga gtctgtttga gaataatgac cttttctatt 120
 tctataaaga cagttttgaa ttcatctatt agcatatgct ggtgcttgcc tgttgacact 180

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agtcactgaa tttaaaggca gaaaatgtta ttgcacattt agtaatcaag tgttcacga      240
agttaacatc tggatgttaa aggactcaga acaagtgtta ctaagcctgc atttttttat      300
ctgttcaaac atgatgtgtt ntctgctcat catttcatca attctggtag agttgcattt      360
gttcttggaa atgtngccaa tggcttcata gctctagtaa atgtcattga ctgngttaac      420
acacgaaaga tctcctcagc tgagcaaatt ctactgctc tggtggtctc cagaattggt      480
nntactctgn gtcatagtat tccttgagat gcaactagat gttaatctgc tctatatagg      540
ntagaagtaa gaattgttgc ttctaatgcc tgagctcgta cgaaccatt      589

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<210> 44

<211> 314

<212> PRT

<213> Homo sapiens

<400> 44

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Met Ala Thr Glu Leu Asp Lys Ile Phe Leu Ile Leu Ala Ile Ala Glu
1          5          10          15

Phe Ile Ile Ser Met Leu Gly Asn Val Phe Ile Gly Leu Val Asn Cys
          20          25          30

Ser Glu Gly Ile Lys Asn Gln Lys Val Phe Ser Ala Asp Phe Ile Leu
          35          40          45

Thr Cys Leu Ala Ile Ser Thr Ile Gly Gln Leu Leu Val Ile Leu Phe
          50          55          60

Asp Ser Phe Leu Val Gly Leu Ala Ser His Leu Tyr Thr Thr Tyr Arg
65          70          75          80

Leu Gly Lys Thr Val Ile Met Leu Trp His Met Thr Asn His Leu Thr
          85          90          95

Thr Trp Leu Ala Thr Cys Leu Ser Ile Phe Tyr Phe Phe Lys Ile Ala
          100          105          110

His Phe Pro His Ser Leu Phe Leu Trp Leu Arg Trp Arg Met Asn Gly
          115          120          125

Met Ile Val Met Leu Leu Ile Leu Ser Leu Phe Leu Leu Ile Phe Asp
          130          135          140

Ser Leu Val Leu Glu Ile Phe Ile Asp Ile Ser Leu Asn Ile Ile Asp
145          150          155          160

Lys Ser Asn Leu Thr Leu Tyr Leu Asp Glu Ser Lys Thr Leu Tyr Asp
          165          170          175

Lys Leu Ser Ile Leu Lys Thr Leu Leu Ser Leu Thr Ser Phe Ile Pro
          180          185          190

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Phe Ser Leu Phe Leu Thr Ser Leu Leu Phe Leu Phe Leu Ser Leu Val
 195 200 205
 Arg His Thr Arg Asn Leu Lys Leu Ser Ser Leu Gly Ser Arg Asp Ser
 210 215 220
 Ser Thr Glu Ala His Arg Arg Ala Met Lys Met Val Met Ser Phe Leu
 225 230 235 240
 Phe Leu Phe Ile Val His Phe Phe Ser Leu Gln Val Ala Asn Gly Ile
 245 250 255
 Phe Phe Met Leu Trp Asn Asn Lys Tyr Ile Lys Phe Val Met Leu Ala
 260 265 270
 Leu Asn Ala Phe Pro Ser Cys His Ser Phe Ile Leu Ile Leu Gly Asn
 275 280 285
 Ser Lys Leu Arg Gln Thr Ala Val Arg Leu Leu Trp His Leu Arg Asn
 290 295 300
 Tyr Thr Lys Thr Pro Asn Ala Leu Pro Leu
 305 310

<210> 45

<211> 945

<212> DNA

<213> Homo sapiens

<400> 45

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gtctttctcag ctgacttcat cctcacctgc ttggctatct ccacaattgg acaactgttg	180
gtgatactgt ttgattcatt tctagtggga cttgcttcac atttatatac cacatataga	240
ctaggaaaaa ctgttattat gctttggcac atgactaatc acttgacaac ctggcttgcc	300
acctgcctaa gcattttcta tttctttaag atagcccact tccccactc ccttttcctc	360
tggctgaggt ggaggatgaa cggaatgatt gttatgcttc ttatattgtc tttgttctta	420
ctgatttttg acagtttagt gctagaaata tttattgata tctcactcaa tataatagat	480
aaaagtaatc tgactttata tttagatgaa agtaaaactc tctatgataa actctctatt	540
ttaaaaaactc ttctcagctt aaccagtttt atcccccttt ctctgttctt gacctccttg	600
cttttttttat ttctgtcctt ggtgagacat actagaaatt tgaagctcag ttccttgggc	660
tctagagact ccagcacaga ggcccatagg agggccatga aaatgggtgat gtctttcctt	720
ttctctttca tagttcattt tttttcctta caagtggcca atgggatatt ttttatgttg	780
tggaacaaca agtacataaa gtttgtcatg ttagccttaa atgcctttcc ctcgtgccac	840

tcattttattc tcattctctggg aaacagcaag ctgcgacaga cagctgtgag gctactgtgg 900

catcttagga actatacaaaa aacaccaaatt gctttacctt tgtag 945

<210> 46

<211> 72

<212> PRT

<213> Homo sapiens

<400> 46

Leu Ser Pro Phe Arg Met Leu Phe Ala Ile Tyr Phe Leu Cys Ile Ile
1 5 10 15

Thr Ser Thr Trp Asn Pro Arg Thr Gln Gln Ser Asn Leu Val Phe Leu
20 25 30

Leu Tyr Gln Thr Leu Ala Ile Met Tyr Pro Ser Phe His Ser Phe Ile
35 40 45

Leu Ile Met Arg Ser Arg Lys Leu Lys Gln Thr Ser Leu Ser Val Leu
50 55 60

Cys Gln Val Thr Cys Trp Val Lys
65 70

<210> 47

<211> 263

<212> PRT

<213> Homo sapiens

<400> 47

Met Pro Pro Gly Ile Gly Asn Thr Phe Leu Ile Val Met Met Gly Glu
1 5 10 15

Phe Ile Ile Met Leu Gly Asn Gly Phe Ile Val Leu Val Asn Cys Ile
20 25 30

Asp Val Arg Ser Gln Met Ile Leu Leu Asp Asn Cys Ile Leu Thr Ser
35 40 45

Leu Ala Ile Ser Thr Ile Ser Gln Leu Trp Ile Ile Leu Leu Asp Ser
50 55 60

Phe Val Thr Ala Leu Trp Pro His Leu Tyr Ala Phe Asn Lys Leu Ile
65 70 75 80

Lys Phe Ile His Ile Phe Trp Ala Leu Thr Asn His Leu Val Thr Trp
85 90 95

Leu Ala Cys Cys Leu Ser Val Phe Tyr Phe Phe Lys Ile Ala Tyr Phe
100 105 110

Ser His Pro Cys Phe Ile Trp Leu Arg Trp Arg Ile Ser Arg Thr Leu
115 120 125

Leu Glu Leu Pro Leu Gly Ser Leu Leu Leu Leu Phe Phe Asn Leu Ala
 130 135 140
 Leu Thr Gly Gly Leu Ser Asp Leu Trp Ile Asn Ile Tyr Thr Met Tyr
 145 150 155 160
 Glu Arg Asn Ser Thr Trp Ser Leu Asp Val Ser Lys Ile Leu Tyr Cys
 165 170 175
 Ser Leu Trp Ile Leu Val Ser Leu Ile Tyr Leu Ile Ser Phe Leu Leu
 180 185 190
 Ser Leu Ile Ser Leu Leu Leu Leu Ile Leu Ser Leu Met Arg His Ile
 195 200 205
 Arg Asn Leu Gln Leu Asn Thr Met Gly Pro Arg Asp Leu Arg Met Lys
 210 215 220
 Ala His Lys Arg Ala Met Lys Met Lys Met Lys Met Met Val Ser Phe
 225 230 235 240
 Leu Leu Phe Phe Leu Val His Phe Ser Ser Leu Leu Pro Thr Gly Trp
 245 250 255
 Ile Phe Leu Ile Gln Gln Lys
 260

<210> 48
 <211> 258
 <212> PRT
 <213> Homo sapiens

<400> 48
 Leu Ala Asn Leu Ile Asp Trp Ala Glu Asn Gln Ile Cys Leu Met Asp
 1 5 10 15
 Phe Ile Leu Ser Ser Leu Ala Ile Cys Arg Thr Leu Leu Leu Gly Cys
 20 25 30
 Cys Val Ala Ile Arg Cys Thr Tyr Asn Asp Tyr Pro Asn Ile Asp Ala
 35 40 45
 Val Asn His Asn Leu Ile Lys Ile Ile Thr Ile Phe Asp Ile Leu Arg
 50 55 60
 Leu Val Ser Lys Leu Gly Ile Trp Phe Ala Ser Tyr Leu Ser Ile Phe
 65 70 75 80
 Tyr Leu Leu Lys Val Ala Leu Phe His His Ala Ile Phe Leu Trp Leu
 85 90 95
 Lys Trp Arg Ile Ser Arg Ala Val Phe Thr Phe Leu Met Ile Phe Leu
 100 105 110
 Phe Phe Tyr Ile Ser Ile Ile Ser Met Ile Lys Ile Lys Leu Phe Leu
 115 120 125

Asp Gln Cys Tyr Lys Ile Glu Lys Leu Leu Leu Glu Gly Arg Cys Glu
 130 135 140
 Ser Pro Pro Ser Cys Pro Asp Ala His Pro Gly Val Val Tyr Ser Leu
 145 150 155 160
 Tyr His Phe Ser Tyr Leu Met Phe Leu Val Cys Tyr Leu Pro Lys Gly
 165 170 175
 Lys His Cys Thr Ala Val Val Ile Gly Asp Trp Leu Gln Arg Pro Arg
 180 185 190
 Thr Glu Ala Tyr Val Arg Ala Met Asn Ile Met Ile Ala Phe Phe Phe
 195 200 205
 His Leu Leu Tyr Ser Leu Gly Thr Ser Leu Ser Ser Val Ser Tyr Phe
 210 215 220
 Leu Cys Lys Arg Lys Ile Val Ala Leu Gly Ala Tyr Leu Ser Tyr Pro
 225 230 235 240
 Leu Ser His Ser Phe Ile Leu Ile Met Glu Asn Asn Lys Val Arg Lys
 245 250 255

Ala Leu

<210> 49
 <211> 35
 <212> PRT
 <213> Homo sapiens

<400> 49
 Asn Ile Cys Val Leu Leu Ile Ile Leu Ser Ile Leu Val Val Ser Ala
 1 5 10 15
 Phe Val Leu Gly Asn Val Ala Asn Gly Phe Ile Ala Leu Ile Asn Val
 20 25 30

Asn Asp Trp
 35

<210> 50
 <211> 36
 <212> PRT
 <213> Homo sapiens

<400> 50
 Met Gln Ala Ala Leu Thr Ala Phe Phe Val Leu Leu Phe Ser Leu Leu
 1 5 10 15
 Ser Leu Leu Gly Ile Ala Ala Asn Gly Phe Ile Val Leu Val Leu Gly
 20 25 30

Lys Glu Trp Leu
 35

<210> 51
 <211> 319
 <212> PRT
 <213> Homo sapiens

<400> 51
 Met Ile Thr Phe Leu Pro Ile Ile Phe Ser Ile Leu Val Val Val Thr
 1 5 10 15
 Phe Val Leu Gly Asn Phe Ser Asn Gly Phe Ile Ala Leu Val Asn Ser
 20 25 30
 Ile Glu Trp Val Lys Thr Arg Lys Ile Ser Ser Ala Asp Gln Ile Leu
 35 40 45
 Thr Ala Leu Val Val Ser Arg Val Gly Leu Leu Trp Val Ile Leu Leu
 50 55 60
 His Trp Tyr Ala Asn Val Phe Asn Ser Ala Leu Tyr Ser Ser Glu Val
 65 70 75 80
 Gly Ala Val Ala Ser Asn Ile Ser Ala Ile Ile Asn His Phe Ser Ile
 85 90 95
 Trp Leu Ala Thr Ser Leu Ser Ile Phe Tyr Leu Leu Lys Ile Ala Asn
 100 105 110
 Phe Ser Asn Leu Ile Phe Leu His Leu Lys Lys Arg Ile Arg Ser Val
 115 120 125
 Val Leu Val Ile Leu Leu Gly Pro Leu Val Phe Leu Ile Cys Asn Leu
 130 135 140
 Ala Val Ile Thr Met Asp Asp Ser Val Trp Thr Lys Glu Tyr Glu Gly
 145 150 155 160
 Asn Val Thr Trp Lys Ile Lys Leu Arg Asn Ala Ile His Leu Ser Asn
 165 170 175
 Met Thr Val Ser Thr Leu Ala Asn Leu Ile Pro Phe Ile Leu Thr Leu
 180 185 190
 Ile Cys Phe Leu Leu Leu Ile Cys Ser Leu Cys Lys His Leu Lys Lys
 195 200 205
 Met Gln Leu His Gly Lys Gly Ser Gln Asp Pro Ser Thr Lys Val His
 210 215 220
 Ile Lys Ala Leu Gln Thr Val Thr Ser Phe Leu Leu Leu Cys Ala Ile
 225 230 235 240
 Tyr Phe Leu Ser Met Ile Ile Ser Val Cys Asn Phe Gly Arg Leu Glu
 245 250 255
 Lys Gln Pro Val Phe Met Phe Cys Gln Ala Ile Ile Phe Ser Tyr Pro
 260 265 270

Ser Thr His Pro Phe Ile Leu Ile Leu Gly Asn Lys Lys Leu Lys Gln
 275 280 285

Ile Phe Leu Ser Val Leu Arg His Val Arg Tyr Trp Val Lys Asp Arg
 290 295 300

Ser Leu Arg Leu His Arg Phe Thr Arg Gly Ala Leu Cys Val Phe
 305 310 315

<210> 52
 <211> 960
 <212> DNA
 <213> Homo sapiens

<400> 52
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 aattttttcca atggcttcat agctctagta aattccattg agtgggtcaa gacacgaaag 120
 atctcctcag ctgaccaaat cctcactgct ctgggtggtct ccagagttgg ttactctgg 180
 gtcataattat tacattggta tgcaaagtgt tttaattcag ctttatatag ttcagaagta 240
 ggagctgttg cttctaatat ctcagcaata atcaaccatt tcagcatctg gcttgctact 300
 agcctcagca tattttatct gctcaagatt gccaatctct ccaaccttat tttctctcac 360
 ttaaagaaga gaattaggag tgttggtctg gtgatactgt tgggtccctt ggtatttttg 420
 atttgtaatc ttgctgtgat aaccatggat gacagtgtgt ggacaaaaga atatgaagga 480
 aatgtgactt ggaagatcaa attgaggaat gcaatacacc tttcaaatat gactgtaagc 540
 acactagcaa acctcatacc cttcattctg accctaatat gttttctgct gttaatctgt 600
 tctctgtgta aacatctcaa gaagatgcag ctccatggca aaggatctca agatcccagc 660
 accaaggtcc acataaaagc tttgcaaact gtgacctcct ttcttctggt atgtgccatt 720
 tactttctgt ccatgatcat atcagtttgt aattttggga ggctggaaaa gcaacctgtc 780
 ttcatgttct gccaaagctat tatattcagc tacccttcaa cccaccttatt catcctgatt 840
 ttgggaaaca agaagctaaa gcagatcttt ctttcagttt tgcggcatgt gaggtactgg 900
 gtgaaagaca gaagccttcg tctccataga ttcacaagag gggcattgtg tgtcttctag 960

<210> 53
 <211> 299
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MOD_RES
 <222> (176)..(176)
 <223> Variable amino acid

<220>

<221> MOD_RES

<222> (184)..(184)

<223> Variable amino acid

<400> 53

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Met Thr Thr Phe Ile Pro Ile Ile Phe Ser Ser Val Val Val Val Leu
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Phe Val Ile Gly Asn Phe Ala Asn Gly Phe Ile Ala Leu Val Asn Ser
20          25          30

Ile Glu Arg Val Lys Arg Gln Lys Ile Ser Phe Ala Asp Gln Ile Leu
35          40          45

Thr Ala Leu Ala Val Ser Arg Val Gly Leu Leu Trp Val Leu Leu Leu
50          55          60

Asn Trp Tyr Ser Thr Val Phe Asn Pro Ala Phe Tyr Ser Val Glu Val
65          70          75          80

Arg Thr Thr Ala Tyr Asn Val Trp Ala Val Thr Gly His Phe Ser Asn
85          90          95

Trp Leu Ala Thr Ser Leu Ser Ile Phe Tyr Leu Leu Lys Ile Ala Asn
100         105         110

Phe Ser Asn Leu Ile Phe Leu His Leu Lys Arg Arg Val Lys Ser Val
115         120         125

Ile Leu Val Met Leu Leu Gly Pro Leu Leu Phe Leu Ala Cys Gln Leu
130         135         140

Phe Val Ile Asn Met Lys Glu Ile Val Arg Thr Lys Glu Phe Glu Gly
145         150         155         160

Asn Met Thr Trp Lys Ile Lys Leu Lys Ser Ala Met Tyr Phe Ser Xaa
165         170         175

Met Thr Val Thr Ile Gly Ala Xaa Leu Val Pro Phe Thr Leu Ser Leu
180         185         190

Ile Ser Phe Leu Met Leu Ile Cys Ser Leu Cys Lys His Leu Lys Lys
195         200         205

Met Gln Leu His Gly Glu Gly Ser Gln Asp Leu Ser Thr Lys Val His
210         215         220

Ile Lys Ala Leu Gln Thr Leu Ile Ser Phe Leu Leu Leu Cys Ala Ile
225         230         235         240

Phe Phe Leu Phe Leu Ile Val Ser Val Trp Ser Pro Arg Arg Leu Arg
245         250         255

Asn Asp Pro Val Val Met Val Ser Lys Ala Val Gly Asn Ile Tyr Leu
260         265         270

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Ala Phe Asp Ser Phe Ile Leu Ile Trp Arg Thr Lys Lys Leu Lys His
 275 280 285

Thr Phe Leu Leu Ile Leu Cys Gln Ile Arg Cys
 290 295

<210> 54
 <211> 900
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (526)..(526)
 <223> n is a, c, g, or t

<220>
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 <222> (550)..(550)
 <223> n is a, c, g, or t

<400> 54
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 atctcttttg ctgaccagat tctcactgct ctggcggctc ccagagttgg tttgctctgg 180
 gtattattat taaattggta ttcaactgtg tttaatccag ctttttatag tgtagaagta 240
 agaactactg cttataatgt ctgggcagta accggccatt tcagcaactg gcttgctact 300
 agcctcagca tatttttattt gctcaagatt gccaatctct ccaaccttat ttttcttcac 360
 ttaaagagga gagttaagag tgtcattctg gtgatgctgt tggggccttt actatttttg 420
 gcttgctcaac tttttgtgat aaacatgaaa gagattgtac ggacaaaaga atttgaagga 480
 aacatgactt ggaagatcaa attgaagagt gcaatgtact tttcanatat gactgtaacc 540
 attggagcan acttagtacc ctttactctg tccctgatat cttttctgat gctaattctgt 600
 tctctgtgta aacatctcaa gaagatgcag ctccatggag aaggatcgca agatctcagc 660
 accaagggtcc acataaaagc tttgcaaact ctgatctcct tcctcttggt atgtgccatt 720
 ttctttctat tcctaactgt ttcggtttgg agtcctagga ggctgcgga tgacccggtt 780
 gtcatgggta gcaaggctgt tggaaacata tatcttgcac tcgaactcatt catcctaatt 840
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<210> 55
 <211> 20
 <212> PRT
 <213> Homo sapiens

<400> 55

His Ser Phe Met Leu Thr Met Gly Ser Arg Lys Pro Lys Gln Thr Phe
 1 5 10 15

Leu Ser Ala Leu
 20

<210> 56

<211> 309

<212> PRT

<213> Homo sapiens

<400> 56

Met Val Tyr Phe Leu Pro Ile Ile Phe Ser Ile Leu Val Val Phe Ala
 1 5 10 15

Phe Val Leu Gly Asn Phe Ser Asn Gly Phe Ile Ala Leu Val Asn Val
 20 25 30

Ile Asp Trp Val Lys Arg Gln Lys Ile Ser Ser Ala Asp Gln Ile Leu
 35 40 45

Thr Ala Leu Val Val Ser Arg Val Gly Leu Leu Trp Val Ile Leu Leu
 50 55 60

His Trp Tyr Ala Asn Val Phe Asn Ser Ala Leu Tyr Ser Leu Glu Val
 65 70 75 80

Arg Ile Val Ala Ser Asn Ile Ser Ala Val Ile Asn His Phe Ser Ile
 85 90 95

Trp Leu Ala Ala Ser Leu Ser Ile Phe Tyr Leu Leu Lys Ile Ala Asn
 100 105 110

Phe Ser Asn Leu Ile Phe Leu His Leu Lys Lys Arg Ile Lys Ser Val
 115 120 125

Val Leu Val Ile Leu Leu Gly Pro Leu Val Phe Leu Ile Cys Asn Leu
 130 135 140

Ala Val Ile Thr Met Asp Glu Arg Val Trp Thr Lys Glu Tyr Glu Gly
 145 150 155 160

Asn Val Thr Trp Lys Ile Lys Leu Arg Asn Ala Ile His Leu Ser Ser
 165 170 175

Leu Thr Val Thr Thr Leu Ala Asn Leu Ile Pro Phe Thr Leu Ser Leu
 180 185 190

Ile Cys Phe Leu Leu Leu Ile Cys Ser Leu Cys Lys His Leu Lys Lys
 195 200 205

Met Gln Leu His Ser Lys Gly Ser Gln Asp Pro Ser Thr Lys Val His
 210 215 220

Ile Lys Ala Leu Gln Thr Val Ile Ser Phe Leu Met Leu Cys Ala Ile
 225 230 235 240
 Tyr Phe Leu Ser Ile Met Ile Ser Val Met Asn Leu Arg Ser Leu Glu
 245 250 255
 Asn Lys Pro Val Phe Met Phe Cys Lys Ala Ile Arg Phe Ser Tyr Pro
 260 265 270
 Ser Ile His Pro Phe Ile Leu Ile Trp Gly Asn Lys Lys Leu Lys Gln
 275 280 285
 Thr Phe Leu Ser Val Phe Trp Gln Val Arg Tyr Trp Val Lys Gly Glu
 290 295 300
 Lys Pro Ser Ser Pro
 305

<210> 57

<211> 930

<212> DNA

<213> Homo sapiens

<400> 57

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atctcctcag ctgaccaaatt tctcactgct ctgggtggtct ccagagttgg tttactctgg	180
gtcatattat tacattggta tgcaaatgtg tttaattcag ctttatatag tttagaagta	240
agaattgttg cttctaatat ctgagcagta atcaaccatt tcagcatctg gcttgctgct	300
agcctcagca tatttttattt gctcaagatt gccaatctct ccaaccttat ttttctccac	360
ctaaagaaga gaattaagag tggtgttctg gtgatactgt tggggccctt ggtatttctg	420
atgtgtaatc ttgctgtgat aaccatggat gagagagtgt ggacaaaaga atatgaagga	480
aatgtgactt ggaagatcaa attgaggaat gcaatacacc tttcaagctt gactgtaact	540
actctagcaa acctcatacc ctttactctg agcctaatat gttttctgct gttaatctgt	600
tctcttttga aacatctcaa gaagatgcag ctccatagca aaggatctca agatcccagc	660
accaaggtcc acataaaagc ttgcaaaact gtgatctcct tctcatggtt atgtgccatt	720
tactttctgt ccataatgat atcagtttgg aatcttagga gtctggaaaa caaacctgtc	780
ttcatgttct gcaaagctat tagattcagc tatccttcaa tccaccatt catcctgatt	840
tggggaaaca agaagctaaa gcagactttt ctttcagttt tttggcaagt gaggtactgg	900
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<210> 58
 <211> 100
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (5)..(5)
 <223> Variable amino acid

<220>
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 <223> Variable amino acid

<220>
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 <222> (71)..(71)
 <223> Variable amino acid

<220>
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 <222> (85)..(85)
 <223> Variable amino acid

<400> 58
 Gly Ser Ser Arg Xaa Lys Pro Pro Arg Ile Pro His Lys Lys Leu Cys
 1 5 10 15
 Lys Leu Gly Pro Ser Phe Pro His Asn Asn Leu Pro Ile Tyr Phe Leu
 20 25 30
 Cys Xaa Asn His Ile Val Leu Glu Phe Leu Lys Met Arg Pro Lys Lys
 35 40 45
 Lys Cys Ser Leu Met Leu Cys Gln Ala Phe Gly Ile Ile Tyr Pro Ser
 50 55 60
 Phe His Ser Phe Ile Leu Xaa Trp Gly Asn Lys Thr Leu Lys Gln Thr
 65 70 75 80
 Phe Leu Ser Val Xaa Trp Gln Val Thr Cys Trp Ala Lys Gly Gln Asn
 85 90 95
 Gln Ser Thr Pro
 100

<210> 59
 <211> 128
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MOD_RES
 <222> (62)..(62)
 <223> Variable amino acid

<220>
 <221> MOD_RES
 <222> (72)..(72)
 <223> Variable amino acid

<400> 59

Asn	Ala	Ile	Arg	Pro	Ser	Lys	Leu	Trp	Thr	Val	Thr	Glu	Ala	Asp	Lys
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Thr	Ser	Gln	Pro	Gly	Thr	Ser	Ala	Asn	Lys	Ile	Phe	Ser	Ala	Gly	Asn
			20					25					30		
Leu	Ile	Ser	His	Val	Asn	Met	Ser	Arg	Arg	Met	Gln	Leu	His	Gly	Lys
		35					40					45			
Gly	Ser	Gln	His	Leu	Ser	Thr	Arg	Val	His	Ile	Lys	Ala	Xaa	Gln	Thr
	50					55					60				
Val	Ile	Ser	Phe	Leu	Met	Leu	Xaa	Ala	Ile	Tyr	Phe	Leu	Cys	Leu	Ile
65					70					75				80	
Thr	Ser	Thr	Trp	Asn	Pro	Arg	Thr	Gln	Gln	Ser	Lys	Leu	Val	Phe	Leu
				85					90					95	
Leu	Tyr	Gln	Thr	Leu	Gly	Phe	Met	Tyr	Leu	Leu	Phe	His	Ser	Phe	Ile
		100						105					110		
Leu	Thr	Met	Gly	Ser	Arg	Lys	Pro	Lys	Gln	Thr	Phe	Leu	Ser	Ala	Leu
		115					120					125			

<210> 60
 <211> 309
 <212> PRT
 <213> Homo sapiens

<400> 60

Met	Ile	Cys	Phe	Leu	Leu	Ile	Ile	Leu	Ser	Ile	Leu	Val	Val	Phe	Ala
1				5				10						15	
Phe	Val	Leu	Gly	Asn	Phe	Ser	Asn	Gly	Phe	Ile	Ala	Leu	Val	Asn	Val
			20					25					30		
Ile	Asp	Trp	Val	Lys	Arg	Gln	Lys	Ile	Ser	Ser	Ala	Asp	Gln	Ile	Leu
		35					40					45			
Thr	Ala	Leu	Val	Val	Ser	Arg	Val	Gly	Leu	Leu	Trp	Val	Ile	Leu	Leu
	50					55					60				
His	Trp	Tyr	Ser	Asn	Val	Leu	Asn	Ser	Ala	Leu	Tyr	Ser	Ser	Glu	Val
65					70					75				80	
Ile	Ile	Phe	Ile	Ser	Asn	Ala	Trp	Ala	Ile	Ile	Asn	His	Phe	Ser	Ile
				85				90					95		
Trp	Leu	Ala	Thr	Ser	Leu	Ser	Ile	Phe	Tyr	Leu	Leu	Lys	Ile	Val	Asn
		100						105					110		

Phe Ser Arg Leu Ile Phe His His Leu Lys Arg Lys Ala Lys Ser Val
 115 120 125
 Val Leu Val Ile Val Leu Gly Pro Leu Val Phe Leu Val Cys His Leu
 130 135 140
 Val Met Lys His Thr Tyr Ile Asn Val Trp Thr Lys Glu Tyr Glu Gly
 145 150 155 160
 Asn Val Thr Trp Lys Ile Lys Leu Arg Asn Ala Ile His Leu Ser Asn
 165 170 175
 Leu Thr Val Ser Thr Leu Ala Asn Leu Ile Pro Phe Thr Leu Thr Leu
 180 185 190
 Ile Ser Phe Leu Leu Leu Ile Tyr Ser Leu Cys Lys His Leu Lys Lys
 195 200 205
 Met Gln Leu His Gly Lys Gly Ser Gln Asp Pro Ser Thr Lys Val His
 210 215 220
 Ile Lys Ala Leu Gln Thr Val Thr Ser Phe Leu Leu Leu Cys Ala Ile
 225 230 235 240
 Tyr Phe Leu Ser Met Ile Ile Ser Val Cys Asn Phe Gly Arg Leu Glu
 245 250 255
 Lys Gln Pro Val Phe Met Phe Cys Gln Ala Ile Ile Phe Ser Tyr Pro
 260 265 270
 Ser Thr His Pro Phe Ile Leu Ile Leu Gly Asn Lys Lys Leu Lys Gln
 275 280 285
 Ile Phe Leu Ser Val Phe Trp Gln Met Arg Tyr Trp Val Lys Gly Glu
 290 295 300
 Lys Pro Ser Ser Pro
 305

<210> 61

<211> 930

<212> DNA

<213> Homo sapiens

<400> 61

atgatatgtt ttctgctcat cattttatca attctggtag tgtttgcatt tgttcttgga	60
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atctcctcag ctgaccaaatt cctcactgct ctggtggtct ccagagttgg ttactctgg	180
gtaatattat tacattggta ttcaaattgtg ttgaattcag ctttatatag ttcagaagta	240
ataatttttta tttctaattgc ctgggcaata atcaaccatt tcagcatctg gcttgctact	300
agcctcagca tattttattt gctcaagatc gtcaatttct ccagacttat ttttcatcac	360

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ttaaaaagga aggctaagag tgtagttctg gtgatagtgt tgggtccctt ggtatTTTTg 420
gtttgtcacc ttgtgatgaa acacacgtat ataaatgtgt ggacaaaaga atatgaagga 480
aatgtgactt ggaagatcaa actgaggaat gcaatacacc tttcaaactt gactgtaagc 540
aactagcaa acttgatacc cttcactctg accctgatat cttttctgct gttaatctac 600
tctctgtgta aacatctcaa gaagatgcag ctccatggca aaggatctca agatcccagc 660
accaaggtcc acataaaagc ttgcaaaact gtgacctcct ttcttctggt atgtgccatt 720
tactttctgt ccatgatcat atcagtttgt aattttggga ggctggaaaa gcaacctgtc 780
ttcatgttct gccaaagtat tatattcagc tacccttcaa cccaccatt catcctgatt 840
ttgggaaaca agaagctaaa gcagattttt ctttcagttt tttggcaaat gaggtactgg 900
gtgaaaggag agaagccttc atctccatag 930

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<210> 62

<211> 306

<212> PRT

<213> Homo sapiens

<400> 62

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Met Ile Thr Phe Leu Pro Ile Ile Phe Ser Ile Leu Ile Val Val Thr
1           5           10           15

Phe Val Ile Gly Asn Phe Ala Asn Gly Phe Ile Ala Leu Val Asn Ser
20           25           30

Ile Glu Trp Val Lys Arg Gln Lys Ile Ser Ser Ala Asp Gln Ile Ser
35           40           45

His Cys Ser Gly Gly Val Gln Asn Trp Phe Thr Leu Gly His Ile Ile
50           55           60

Thr Leu Val Cys Asn Cys Val Phe Gly Phe Ile Ile Arg Ser Lys Asn
65           70           75           80

Phe Trp Phe Cys Leu Ser Asn Asn Gln Ala Phe Gln His Val Gly Val
85           90           95

Thr Ser Leu Ser Ile Phe His Leu Leu Lys Thr Ala Asn Phe Ser Asn
100          105          110

Leu Ile Phe Leu His Leu Lys Lys Arg Ile Lys Ser Val Gly Leu Val
115          120          125

Ile Leu Leu Gly Pro Leu Leu Phe Phe Ile Cys Asn Leu Phe Val Ile
130          135          140

Asn Met Asp Glu Ser Val Trp Thr Lys Glu Tyr Glu Gly Asn Val Thr
145          150          155          160

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Trp	Lys	Ile	Lys	Leu	Arg	Ser	Ala	Met	Tyr	His	Ser	Asn	Met	Thr	Leu		
				165					170					175			
Thr	Met	Leu	Ala	Asn	Phe	Val	Pro	Phe	Thr	Leu	Thr	Leu	Ile	Ser	Phe		
				180					185					190			
Leu	Leu	Leu	Ile	Cys	Ser	Leu	Cys	Lys	His	Leu	Lys	Lys	Met	Gln	Leu		
				195					200					205			
His	Gly	Lys	Gly	Ser	Gln	Asp	Pro	Ser	Thr	Lys	Val	His	Ile	Lys	Ala		
				210					215					220			
Leu	Gln	Thr	Val	Thr	Ser	Phe	Leu	Leu	Leu	Cys	Ala	Ile	Tyr	Phe	Leu		
225								230					235				
Ser	Met	Ile	Ile	Ser	Val	Cys	Asn	Leu	Gly	Arg	Leu	Glu	Lys	Gln	Pro		
				245					250					255			
Val	Phe	Met	Phe	Cys	Glu	Ala	Ile	Ile	Phe	Ser	Tyr	Pro	Ser	Thr	His		
				260					265					270			
Pro	Phe	Ile	Leu	Ile	Leu	Gly	Asn	Lys	Lys	Leu	Lys	Gln	Ile	Phe	Leu		
				275					280					285			
Ser	Val	Leu	Arg	His	Val	Arg	Tyr	Trp	Val	Lys	Gly	Glu	Lys	Pro	Ser		
				290					295					300			
Ser	Ser																
305																	

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<210> 63
<211> 930
<212> DNA
<213> Homo sapiens
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<400>	63						
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atctcatcag	ctgaccaa	ttctcactgc	tctgggtggtg	tccagaattg	gtttactctg		180
ggtcataatta	ttacattggt	atgcaactgt	gtttaatttg	gcttcatata	gattagaagt		240
aagaatTTTT	ggttctaata	tctcagcaat	aaccaagcat	ttcagcatgt	gggtgttact		300
agcctcagca	tatttcattt	gctcaagact	gccaatttct	ccaaccttat	ttttctccac		360
ctaaagaaga	ggattaagag	tggttggttg	gtgatactat	tggggccttt	gctatttttc		420
atttgtaatc	tttttgat	aaacatggat	gagagtgtat	ggacaaaaga	atatgaagga		480
aacgtgactt	ggaagatcaa	attgaggagt	gcaatgtacc	attcaaatat	gactctaacc		540
atgctagcaa	actttgtacc	cttcactctg	accctgatat	cttttctgct	gttaatctgt		600
tctctgtgta	aacatctcaa	gaagatgcag	ctccatggca	aaggatctca	agatcccagc		660

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accaaggtcc acataaaagc ttgcaaact gtgacctcct ttctttctgtt atgtgccatt 720
tactttctgt ccatgatcat atcagtttgt aatttgggga ggctggaaaa gcaacctgtc 780
ttcatgttct gcgaagctat tatattcagc tctccttcaa cccacccatt catcctgatt 840
ttgggaaaca agaagctaaa gcagattttt ctttcagttt tgcggcatgt gaggtactgg 900
gtgaaaggag agaagccttc atcttcatag 930

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<210> 64
<211> 144
<212> PRT
<213> Homo sapiens

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<400> 64
Met Leu Thr Leu Thr Arg Ile Arg Thr Val Ser Tyr Glu Val Arg Ser
1          5          10          15

Thr Phe Leu Phe Ile Ser Val Leu Glu Phe Ala Val Gly Phe Leu Thr
          20          25          30

Asn Ala Phe Val Phe Leu Val Asn Phe Trp Asp Val Val Lys Arg Gln
          35          40          45

Pro Leu Ser Asn Ser Asp Cys Val Leu Leu Cys Leu Ser Ile Ser Arg
          50          55          60

Leu Phe Leu His Gly Leu Leu Phe Leu Ser Ala Ile Gln Leu Thr His
65          70          75          80

Phe Gln Lys Leu Ser Glu Pro Leu Asn His Ser Tyr Gln Ala Ile Ile
          85          90          95

Met Leu Trp Met Ile Ala Asn Gln Ala Asn Leu Trp Leu Ala Ala Cys
          100          105          110

Leu Ser Leu Leu Tyr Cys Ser Lys Leu Ile Arg Phe Ser His Thr Phe
          115          120          125

Leu Ile Cys Leu Ala Ser Trp Ser Pro Gly Arg Ser Pro Val Pro Ser
          130          135          140

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<210> 65
<211> 140
<212> PRT
<213> Homo sapiens

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<400> 65
Leu Arg Asn Ala Gly Leu Asn Asp Ser Asn Ala Lys Leu Val Arg Asn
1          5          10          15

Asn Asp Leu Leu Leu Ile Asn Leu Ile Leu Leu Leu Pro Leu Ser Val
          20          25          30

```

Phe	Val	Met	Cys	Thr	Ser	Met	Leu	Phe	Val	Ser	Leu	Tyr	Lys	His	Met
		35					40					45			
His	Trp	Met	Gln	Ser	Glu	Ser	His	Lys	Leu	Ser	Ser	Ala	Arg	Thr	Glu
	50					55					60				
Ala	His	Ile	Asn	Ala	Leu	Lys	Thr	Val	Thr	Thr	Phe	Phe	Cys	Phe	Phe
65					70					75					80
Val	Ser	Tyr	Phe	Ala	Ala	Phe	Met	Ala	Asn	Met	Thr	Phe	Arg	Ile	Pro
				85					90					95	
Tyr	Arg	Ser	His	Gln	Phe	Phe	Val	Val	Lys	Glu	Ile	Met	Ala	Ala	Tyr
			100					105					110		
Pro	Ala	Gly	His	Ser	Val	Ile	Ile	Val	Leu	Ser	Asn	Ser	Lys	Phe	Lys
		115					120					125			
Asp	Leu	Phe	Arg	Arg	Met	Ile	Cys	Leu	Gln	Lys	Glu				
	130					135					140				

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<210> 66
<211> 71
<212> PRT
<213> Homo sapiens
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<400> 66
Ser Gln Tyr Ser Leu Gly His Ser Tyr Val Val Ile Phe Gly Tyr Gly
1          5          10          15

Gln Met Lys Lys Thr Phe Leu Gly Ile Leu Trp His Leu Lys Cys Gly
20          25          30

Leu Lys Gly Arg Ala Leu Leu Ala Thr Gln Val Gly Leu Arg Glu Lys
35          40          45

Ser Thr Arg Ser Leu Gly Val Ile Phe Leu Ala Ser Ser Tyr Ser Phe
50          55          60

Phe Val Tyr Val Leu Cys His
65          70

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<210> 67
<211> 308
<212> PRT
<213> Homo sapiens
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<400> 67
Met Ile Thr Phe Leu Leu Ile Ile Leu Ser Ile Leu Val Val Phe Ala
1          5          10          15

Phe Val Leu Gly Asn Phe Ser Asn Gly Phe Ile Ala Leu Val Asn Val
          20          25          30

Ile Asp Trp Val Asn Thr Arg Lys Ile Ser Ser Ala Asp Gln Ile Leu
          35          40          45

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Thr Ala Leu Ala Val Ser Arg Val Gly Leu Leu Trp Val Ile Leu Leu
 50 55 60
 His Trp Tyr Ala Asn Val Leu Asn Pro Ala Leu Tyr Ser Ser Glu Val
 65 70 75 80
 Ile Ile Phe Ile Ser Asn Ile Ser Ala Ile Ile Asn His Phe Ser Ile
 85 90 95
 Trp Leu Ala Thr Ser Leu Ser Ile Phe Tyr Leu Leu Lys Ile Val Asn
 100 105 110
 Phe Ser Arg Leu Ile Phe His His Leu Lys Arg Lys Ala Lys Ser Val
 115 120 125
 Val Leu Val Ile Val Leu Gly Pro Leu Val Phe Leu Val Cys His Leu
 130 135 140
 Val Met Lys His Thr Tyr Ile Asn Val Trp Thr Lys Glu Tyr Glu Gly
 145 150 155 160
 Asn Val Thr Trp Lys Ile Lys Leu Arg Asn Ala Ile His Leu Ser Asn
 165 170 175
 Leu Thr Val Ser Thr Leu Ala Asn Leu Ile Pro Phe Thr Leu Thr Leu
 180 185 190
 Ile Ser Phe Leu Leu Leu Ile Cys Ser Leu Cys Lys His Leu Lys Lys
 195 200 205
 Met Gln Leu His Ser Lys Gly Ser Gln Asp Pro Ser Thr Lys Val His
 210 215 220
 Ile Lys Ala Leu Gln Thr Val Thr Ser Phe Leu Met Leu Phe Ala Ile
 225 230 235 240
 Tyr Phe Leu Tyr Leu Ile Thr Ser Thr Trp Asn Leu Thr Gln Gln Ser
 245 250 255
 Lys Leu Val Phe Met Phe Cys Gln Thr Leu Gly Ile Met Tyr Pro Ser
 260 265 270
 Phe His Ser Phe Ile Leu Ile Met Gly Ser Arg Lys Leu Lys Gln Thr
 275 280 285
 Phe Leu Ser Val Leu Cys Gln Val Thr Cys Leu Val Lys Gly Gln Gln
 290 295 300
 Pro Ser Thr Pro
 305

<210> 68

<211> 34

<212> PRT

<213> Homo sapiens

<400> 68

Phe Ile Gly Leu Thr Asp Cys Ile Ala Trp Met Arg Asn Gln Lys Leu
 1 5 10 15

Cys Met Val Gly Phe Ile Leu Thr Arg Met Ala Leu Ala Arg Ile Asn
 20 25 30

Ile Leu

<210> 69

<211> 293

<212> PRT

<213> Homo sapiens

<220>

<221> MOD_RES

<222> (75)..(97)

<223> Variable amino acid

<400> 69

Leu Glu Leu Ile Phe Ser Lys Val Val Ala Thr Arg Gly Leu Val Leu
 1 5 10 15

Gly Met Leu Gly Asn Gly Leu Ile Gly Leu Val Asn Cys Ile Glu Trp
 20 25 30

Ala Lys Ser Trp Lys Val Ser Ser Ala Asp Phe Ile Leu Thr Ser Leu
 35 40 45

Ala Ile Val Arg Ile Ile Arg Leu Tyr Leu Ile Leu Phe Asp Ser Phe
 50 55 60

Ile Met Val Leu Ser Pro His Leu Tyr Thr Xaa Xaa Xaa Xaa Xaa Xaa
 65 70 75 80

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 85 90 95

Xaa Ser Leu Ser Ile Phe His Trp Phe Lys Thr Ala Asn Phe Ser Asn
 100 105 110

Leu Ile Phe Leu Pro Leu Lys Glu Glu Asp Asn Val Trp Leu Gly Asp
 115 120 125

Ala Val Gly Ala Leu Gly Ile Phe His Leu Ser Cys Ser Glu Asn His
 130 135 140

Gly Glu Val Cys Gly Gln Lys Asn Met Lys Glu Phe Cys Ser Gly Met
 145 150 155 160

Ile Lys Leu Arg Asn Ala Ile Gln Leu Ser Asn Leu Thr Val Thr Met
 165 170 175

Pro Ala Asn Val Thr Pro Cys Thr Leu Thr Leu Ile Ser Phe Leu Leu
 180 185 190

Leu Ile Tyr Ser Pro Cys Lys His Val Lys Lys Met Gln Leu His Gly
 195 200 205
 Lys Gly Ser Gln His Leu Ser Thr Lys Val His Ile Lys Val Leu Gln
 210 215 220
 Thr Val Ile Ser Phe Phe Leu Leu Cys Ala Ile Tyr Phe Val Ser Val
 225 230 235 240
 Ile Ile Ser Val Trp Ser Phe Lys Asn Leu Glu Asn Lys Pro Val Phe
 245 250 255
 Met Phe Cys Gln Ala Ile Gly Phe Ser Cys Ser Ser Ala His Pro Phe
 260 265 270
 Ile Leu Thr Met Gly Asn Lys Lys Leu Lys Gln Thr Tyr Leu Ser Val
 275 280 285
 Leu Trp Gln Met Arg
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<210> 70
 <211> 319
 <212> PRT
 <213> Homo sapiens

<400> 70
 Met Ile Thr Phe Leu Pro Ile Ile Phe Ser Ile Leu Ile Val Val Ile
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 Phe Val Ile Gly Asn Phe Ala Asn Gly Phe Ile Ala Leu Val Asn Ser
 20 25 30
 Ile Glu Trp Val Lys Arg Gln Lys Ile Ser Phe Val Asp Gln Ile Leu
 35 40 45
 Thr Ala Leu Ala Val Ser Arg Val Gly Leu Leu Trp Val Leu Leu Leu
 50 55 60
 His Trp Tyr Ala Thr Gln Leu Asn Pro Ala Phe Tyr Ser Val Glu Val
 65 70 75 80
 Arg Ile Thr Ala Tyr Asn Val Trp Ala Val Thr Asn His Phe Ser Ser
 85 90 95
 Trp Leu Ala Thr Ser Leu Ser Met Phe Tyr Leu Leu Arg Ile Ala Asn
 100 105 110
 Phe Ser Asn Leu Ile Phe Leu Arg Ile Lys Arg Arg Val Lys Ser Val
 115 120 125
 Val Leu Val Ile Leu Leu Gly Pro Leu Leu Phe Leu Val Cys His Leu
 130 135 140
 Phe Val Ile Asn Met Asp Glu Thr Val Trp Thr Lys Glu Tyr Glu Gly
 145 150 155 160

Asn Val Thr Trp Lys Ile Lys Leu Arg Ser Ala Met Tyr His Ser Asn
 165 170 175
 Met Thr Leu Thr Met Leu Ala Asn Phe Val Pro Leu Thr Leu Thr Leu
 180 185 190
 Ile Ser Phe Leu Leu Leu Ile Cys Ser Leu Cys Lys His Leu Lys Lys
 195 200 205
 Met Gln Leu His Gly Lys Gly Ser Gln Asp Pro Ser Thr Lys Val His
 210 215 220
 Ile Lys Ala Leu Gln Thr Val Thr Ser Phe Leu Leu Leu Cys Ala Ile
 225 230 235 240
 Tyr Phe Leu Ser Met Ile Ile Ser Val Cys Asn Leu Gly Arg Leu Glu
 245 250 255
 Lys Gln Pro Val Phe Met Phe Cys Gln Ala Ile Ile Phe Ser Tyr Pro
 260 265 270
 Ser Thr His Pro Phe Ile Leu Ile Leu Gly Asn Lys Lys Leu Lys Gln
 275 280 285
 Ile Phe Leu Ser Val Leu Arg His Val Arg Tyr Trp Val Lys Asp Arg
 290 295 300
 Ser Leu Arg Leu His Arg Phe Thr Arg Gly Ala Leu Cys Val Phe
 305 310 315

<210> 71
 <211> 314
 <212> PRT
 <213> Homo sapiens

<400> 71
 Met Ala Thr Glu Leu Asp Lys Ile Phe Leu Ile Leu Ala Ile Ala Glu
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 Phe Ile Ile Ser Met Leu Gly Asn Val Phe Ile Gly Leu Val Asn Cys
 20 25 30
 Ser Glu Gly Ile Lys Asn Gln Lys Val Phe Ser Ala Asp Phe Ile Leu
 35 40 45
 Thr Cys Leu Ala Ile Ser Thr Ile Gly Gln Leu Leu Val Ile Leu Phe
 50 55 60
 Asp Ser Phe Leu Val Gly Leu Ala Ser His Leu Tyr Thr Thr Tyr Arg
 65 70 75 80
 Leu Gly Lys Thr Val Ile Met Leu Trp His Met Thr Asn His Leu Thr
 85 90 95
 Thr Trp Leu Ala Thr Cys Leu Ser Ile Phe Tyr Phe Phe Lys Ile Ala
 100 105 110

His Phe Pro His Ser Leu Phe Leu Trp Leu Arg Trp Arg Met Asn Gly
 115 120 125
 Met Ile Val Met Leu Leu Ile Leu Ser Leu Phe Leu Leu Ile Phe Asp
 130 135 140
 Ser Leu Val Leu Glu Ile Phe Ile Asp Ile Ser Leu Asn Ile Ile Asp
 145 150 155 160
 Lys Ser Asn Leu Thr Leu Tyr Leu Asp Glu Ser Lys Thr Leu Tyr Asp
 165 170 175
 Lys Leu Ser Ile Leu Lys Thr Leu Leu Ser Leu Thr Ser Phe Ile Pro
 180 185 190
 Phe Ser Leu Phe Leu Thr Ser Leu Leu Phe Leu Phe Leu Ser Leu Val
 195 200 205
 Arg His Thr Arg Asn Leu Lys Leu Ser Ser Leu Gly Ser Arg Asp Ser
 210 215 220
 Ser Thr Glu Ala His Arg Arg Ala Met Lys Met Val Met Ser Phe Leu
 225 230 235 240
 Phe Leu Phe Ile Val His Phe Phe Ser Leu Gln Val Ala Asn Trp Ile
 245 250 255
 Phe Phe Met Leu Trp Asn Asn Lys Cys Ile Lys Phe Val Met Leu Ala
 260 265 270
 Leu Asn Ala Phe Pro Ser Cys His Ser Phe Ile Leu Ile Leu Gly Asn
 275 280 285
 Ser Lys Leu Gln Gln Thr Ala Val Arg Leu Leu Trp His Leu Arg Asn
 290 295 300
 Tyr Thr Lys Thr Pro Asn Pro Leu Pro Leu
 305 310

<210> 72

<211> 59

<212> PRT

<213> Homo sapiens

<400> 72

Met Ser Phe Leu His Ile Val Phe Ser Ile Leu Val Val Val Ala Phe
 1 5 10 15
 Ile Leu Gly Asn Phe Ala Asn Gly Phe Ile Ala Leu Ile Asn Phe Ile
 20 25 30
 Ala Trp Val Lys Lys Gln Lys Ile Ser Ser Ala Asp Gln Ile Ile Ala
 35 40 45
 Asp Lys Gln Ser Pro Glu Leu Val Cys Ser Gly
 50 55

<210> 73
 <211> 63
 <212> PRT
 <213> Homo sapiens

<400> 73
 Met Leu Asn Ala Leu Tyr Ser Ile Leu Ile Ile Ile Ile Asn Ile Phe
 1 5 10 15
 Leu Ile Gly Ile Leu Gly Asn Gly Phe Ile Thr Leu Val Asn Gly Ile
 20 25 30
 Asp Trp Val Lys Met Lys Arg Ser Ser Ile Leu Thr Ala Leu Thr Ile
 35 40 45
 Ser Arg Ile Cys Leu Ile Ser Val Ile Met Val Arg Trp Phe Ile
 50 55 60

<210> 74
 <211> 60
 <212> PRT
 <213> Homo sapiens

<400> 74
 Val Ser Arg Val Gly Leu Leu Trp Val Ile Leu Leu His Trp Tyr Ser
 1 5 10 15
 Thr Val Leu Asn Pro Thr Ser Ser Asn Leu Lys Val Ile Ile Phe Ile
 20 25 30
 Ser Asn Ala Trp Ala Val Thr Asn His Phe Ser Ile Trp Leu Ala Thr
 35 40 45
 Ser Leu Ser Ile Phe Tyr Leu Leu Lys Ile Val Asn
 50 55 60

<210> 75
 <211> 72
 <212> PRT
 <213> Homo sapiens

<400> 75
 Thr Val Thr Met Leu Ala Asn Leu Val Pro Phe Thr Val Thr Leu Ile
 1 5 10 15
 Ser Phe Leu Leu Leu Val Cys Ser Leu Cys Lys His Leu Lys Lys Met
 20 25 30
 His Leu His Gly Lys Gly Ser Gln Asp Pro Ser Thr Lys Val His Ile
 35 40 45
 Lys Val Leu Gln Thr Val Ile Ser Phe Leu Leu Leu Cys Ala Ile Tyr
 50 55 60

Phe Val Ser Val Ile Ile Ser Ser
65 70

<210> 76

<211> 299

<212> PRT

<213> Homo sapiens

<400> 76

Met	Ile	Thr	Phe	Leu	Pro	Ile	Ile	Phe	Ser	Ile	Leu	Val	Val	Val	Thr	
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			20					25					30			
Thr	Glu	Trp	Val	Lys	Arg	Gln	Lys	Ile	Ser	Phe	Ala	Asp	Gln	Ile	Val	
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Thr	Ala	Leu	Ala	Val	Ser	Arg	Val	Gly	Leu	Leu	Trp	Val	Leu	Leu	Leu	
	50					55					60					
Asn	Trp	Tyr	Ser	Thr	Val	Leu	Asn	Pro	Ala	Phe	Tyr	Ser	Val	Glu	Leu	
65					70					75					80	
Arg	Thr	Thr	Ala	Tyr	Asn	Ile	Trp	Ala	Val	Thr	Gly	His	Phe	Ser	Asn	
				85					90					95		
Trp	Pro	Ala	Thr	Ser	Leu	Ser	Ile	Phe	Tyr	Leu	Leu	Lys	Ile	Ala	Asn	
			100					105					110			
Phe	Ser	Asn	Leu	Ile	Phe	Leu	Arg	Leu	Lys	Arg	Arg	Val	Lys	Ser	Val	
		115					120					125				
Ile	Leu	Val	Val	Leu	Leu	Gly	Pro	Leu	Leu	Phe	Leu	Ala	Cys	His	Leu	
	130					135					140					
Phe	Val	Val	Asn	Met	Asn	Gln	Ile	Val	Trp	Thr	Lys	Glu	Tyr	Glu	Gly	
145					150					155					160	
Asn	Met	Thr	Trp	Lys	Ile	Lys	Leu	Arg	Arg	Ala	Met	Tyr	Leu	Ser	Asp	
				165					170					175		
Thr	Thr	Val	Thr	Met	Leu	Ala	Asn	Leu	Val	Pro	Phe	Thr	Val	Thr	Leu	
			180					185					190			
Ile	Ser	Phe	Leu	Leu	Leu	Val	Cys	Ser	Leu	Cys	Lys	His	Leu	Lys	Lys	
		195					200					205				
Met	Gln	Leu	His	Gly	Lys	Gly	Ser	Gln	Asp	Pro	Ser	Thr	Lys	Val	His	
	210					215					220					
Ile	Lys	Val	Leu	Gln	Thr	Val	Ile	Ser	Phe	Phe	Leu	Leu	Cys	Ala	Ile	
225					230					235					240	
Tyr	Phe	Val	Ser	Val	Ile	Ile	Ser	Val	Trp	Ser	Phe	Lys	Asn	Leu	Glu	
				245					250					255		

Asn Lys Pro Val Phe Met Phe Cys Gln Ala Ile Gly Phe Ser Cys Ser
 260 265 270

Ser Ala His Pro Phe Ile Leu Ile Trp Gly Asn Lys Lys Leu Lys Gln
 275 280 285

Thr Tyr Leu Ser Val Leu Trp Gln Met Arg Tyr
 290 295

<210> 77

<211> 335

<212> PRT

<213> Rattus sp.

<400> 77

Met Met Glu Gly His Ile Leu Phe Phe Phe Leu Val Val Met Val Gln
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Phe Val Thr Gly Val Leu Ala Asn Gly Leu Ile Val Val Val His Ala
 20 25 30

Ile Asp Leu Ile Met Trp Lys Lys Met Ala Pro Leu Asp Leu Leu Leu
 35 40 45

Phe Cys Leu Ala Thr Ser Arg Ile Ile Leu Gln Leu Cys Ile Leu Phe
 50 55 60

Ala Gln Leu Cys Leu Phe Ser Leu Val Arg His Thr Leu Phe Glu Asp
 65 70 75 80

Asn Ile Thr Phe Val Phe Ile Ile Asn Glu Leu Ser Leu Trp Phe Ala
 85 90 95

Thr Trp Leu Gly Val Phe Tyr Cys Ala Lys Ile Ala Thr Ile Pro His
 100 105 110

Pro Leu Phe Leu Trp Leu Lys Met Arg Ile Ser Arg Leu Val Pro Trp
 115 120 125

Leu Ile Leu Gly Ser Val Leu Tyr Val Ile Ile Thr Thr Phe Ile His
 130 135 140

Ser Arg Glu Thr Ser Ala Ile Leu Lys Pro Ile Phe Ile Ser Leu Phe
 145 150 155 160

Pro Lys Asn Ala Thr Gln Val Gly Thr Gly His Ala Thr Leu Leu Ser
 165 170 175

Val Leu Val Leu Gly Leu Thr Leu Pro Leu Phe Ile Phe Thr Val Ala
 180 185 190

Val Leu Leu Leu Ile Tyr Ser Leu Trp Asn Tyr Ser Arg Gln Met Arg
 195 200 205

Thr Met Val Gly Thr Arg Glu Tyr Ser Gly His Ala His Ile Ser Ala
 210 215 220

Met Leu Ser Ile Leu Ser Phe Leu Ile Leu Tyr Leu Ser His Tyr Met
 225 230 235 240

Val Ala Val Leu Ile Ser Thr Gln Val Leu Tyr Leu Gly Ser Arg Thr
 245 250 255

Phe Val Phe Cys Leu Leu Val Ile Gly Met Tyr Pro Ser Ile His Ser
 260 265 270

Ile Val Leu Ile Leu Gly Asn Pro Lys Leu Lys Arg Asn Ala Lys Met
 275 280 285

Phe Ile Val His Cys Lys Cys Cys His Cys Thr Arg Ala Trp Val Thr
 290 295 300

Ser Arg Ser Pro Arg Leu Ser Asp Leu Pro Val Pro Pro Thr His Pro
 305 310 315 320

Ser Ala Asn Lys Thr Ser Cys Ser Glu Ala Cys Ile Met Pro Ser
 325 330 335

<210> 78
 <211> 1331
 <212> DNA
 <213> Rattus sp.

<400> 78
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 gcagtttgtc actgggggtct tggcaaattgg cctcattgtg gttgtccatg ctattgactt 180
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ctaattgtcc agcctgaggt ttaatcctag gtttggtact atttcaaaga gtaaagttga      1140
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gtaaacctca ccttgcaaga tgatgtcact gagaaagcag gacaaatgga gtctaggtcc      1260
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<210> 79
 <211> 333
 <212> PRT
 <213> Rattus sp.

<400> 79

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Met Phe Ser Gln Lys Thr Asn Tyr Ser His Leu Phe Thr Phe Ser Ile
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Ile Phe Tyr Val Glu Ile Val Thr Gly Ile Leu Gly Asn Gly Phe Ile
          20          25          30

Ala Leu Val Asn Ile Met Asp Trp Leu Lys Arg Arg Arg Ile Ser Thr
          35          40          45

Ala Asp Gln Ile Leu Thr Ala Leu Ala Leu Thr Arg Leu Ile Tyr Val
50          55          60

Trp Ser Val Leu Ile Cys Ile Leu Leu Leu Phe Leu Cys Pro His Leu
65          70          75          80

Ser Met Arg Pro Glu Met Phe Thr Ala Ile Gly Val Ile Trp Val Val
          85          90          95

Asp Asn His Phe Ser Ile Trp Leu Ala Thr Cys Leu Gly Val Phe Tyr
          100          105          110

Phe Leu Lys Ile Ala Ser Phe Ser Asn Ser Leu Phe Leu Tyr Leu Lys
          115          120          125

Trp Arg Val Lys Lys Val Val Leu Met Ile Ile Leu Ile Ser Leu Ile
          130          135          140

Phe Leu Met Leu Asn Ile Ser Ser Leu Gly Met Tyr Asp His Phe Ser
          145          150          155          160

Ile Asp Val Tyr Glu Gly Asn Met Ser Tyr Asn Leu Val Asp Ser Thr
          165          170          175

His Phe Pro Arg Ile Phe Leu Phe Thr Asn Ser Ser Lys Val Phe Leu
          180          185          190

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Ile Ala Asn Ser Ser His Val Phe Leu Pro Ile Asn Ser Leu Phe Met
 195 200 205
 Leu Ile Pro Phe Thr Val Ser Leu Val Ala Phe Phe Val Leu Phe Leu
 210 215 220
 Ser Leu Trp Lys His His Lys Lys Met Gln Val Asn Ala Lys Gly Pro
 225 230 235 240
 Arg Asp Ala Ser Thr Met Ala His Thr Lys Ala Leu Gln Ile Gly Phe
 245 250 255
 Ser Phe Leu Leu Leu Tyr Ala Ile Tyr Leu Leu Phe Ile Ile Thr Gly
 260 265 270
 Ile Leu Asn Leu Asp Leu Met Arg Cys Ile Val Ile Leu Leu Phe Asp
 275 280 285
 His Ile Ser Gly Ala Val Phe Ser Ile Ser His Ser Phe Val Leu Ile
 290 295 300
 Leu Gly Asn Ser Lys Leu Arg Gln Ala Thr Leu Ser Val Leu Pro Cys
 305 310 315 320
 Leu Arg Cys Arg Ser Lys Asp Met Asp Thr Val Val Phe
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<210> 80

<211> 2438

<212> DNA

<213> Rattus sp.

<400> 80

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<210> 81
 <211> 299
 <212> PRT
 <213> Rattus sp.

<400> 81

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			20					25					30		
Phe	Arg	Glu	Trp	Met	His	Phe	Gln	Arg	Leu	Ser	Pro	Val	Glu	Ile	Ile
			35				40					45			
Leu	Ile	Ser	Leu	Gly	Ile	Ser	His	Phe	Cys	Leu	Gln	Trp	Thr	Ser	Met
	50					55					60				
Leu	Tyr	Asn	Phe	Gly	Thr	Tyr	Ser	Arg	Pro	Val	Leu	Leu	Phe	Trp	Lys
65					70					75					80
Val	Ser	Val	Val	Trp	Glu	Phe	Met	Asn	Val	Leu	Thr	Phe	Trp	Leu	Thr
				85					90					95	
Ser	Leu	Leu	Ala	Val	Leu	Tyr	Cys	Val	Lys	Val	Ser	Ser	Phe	Ser	His
			100					105					110		
Pro	Val	Phe	Leu	Trp	Leu	Arg	Leu	Lys	Ile	Leu	Lys	Leu	Val	Leu	Trp
		115					120					125			
Leu	Leu	Leu	Gly	Ala	Leu	Ile	Ala	Ser	Cys	Leu	Ser	Ile	Ile	Pro	Ser
	130					135					140				
Val	Val	Lys	Tyr	His	Ile	Gln	Met	Glu	Leu	Leu	Thr	Leu	Asp	His	Leu
145					150					155					160
Pro	Lys	Asn	Ser	Ser	Leu	Ile	Leu	Arg	Leu	Gln	Met	Phe	Glu	Trp	Tyr
				165					170					175	
Phe	Ser	Asn	Pro	Phe	Lys	Met	Ile	Gly	Phe	Gly	Val	Pro	Phe	Leu	Val
			180					185					190		
Phe	Leu	Ile	Ser	Ile	Ile	Leu	Leu	Thr	Val	Ser	Leu	Val	Gln	His	Trp
	195						200					205			
Gly	Gln	Met	Lys	His	Tyr	Ser	Ser	Ser	Ser	Ser	Ser	Leu	Arg	Ala	Gln
	210					215						220			
Cys	Thr	Val	Leu	Lys	Ser	Leu	Ala	Thr	Phe	Phe	Ile	Phe	Phe	Thr	Ser
225					230					235					240
Tyr	Phe	Leu	Thr	Ile	Val	Val	Ser	Phe	Ile	Gly	Thr	Val	Phe	Asp	Lys
				245					250					255	
Lys	Ser	Trp	Phe	Trp	Val	Cys	Glu	Ala	Val	Ile	Tyr	Gly	Leu	Val	Cys
			260					265					270		

Ile His Phe Thr Ser Leu Met Met Ser Asn Pro Thr Leu Lys Lys Ala
 275 280 285

Leu Arg Leu Gln Phe Trp Ser Pro Glu Ser Ser
 290 295

<210> 82

<211> 6552

<212> DNA

<213> Rattus sp.

<220>

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<222> (4087)..(4087)

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<222> (4203)..(4203)

<223> n is a, c, g, or t

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Met Glu Tyr Ala Lys Asn Lys Lys Leu Ser Lys Ile Gly Phe Ile Leu
35          40          45
Ile Gly Leu Ala Ile Ser Arg Ile Gly Val Val Trp Ile Ile Ile Leu
50          55          60
Gln Gly Tyr Met Gln Val Phe Phe Pro His Ile Leu Thr Phe Gly Asn
65          70          75          80
Ile Thr Glu Tyr Ile Thr Tyr Ile Trp Val Phe Leu Asn His Leu Ser
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Val Trp Phe Ala Thr Asn Leu Asn Ile Leu Tyr Phe Leu Lys Ile Ala
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 Thr Cys Phe Leu Leu Ile Val Phe Leu Trp Arg His Ile Arg Gln Met
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 Glu Ala Tyr Ile Lys Ile Phe Ser Pro Gln Leu Leu Ser Pro Ile Asn
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 Val Trp Phe Ala Thr Ser Leu Ser Ile Phe Tyr Phe Leu Lys Ile Ala
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 <213> Rattus sp.

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 35 40 45
 Leu Asp Cys Ile Ile Leu Val Gln Tyr Pro Asp Thr Tyr Asn Arg Gly
 50 55 60
 Lys Glu Met Arg Ile Ile Asp Phe Phe Trp Thr Leu Thr Asn His Leu
 65 70 75 80
 Ser Val Trp Phe Ala Thr Cys Leu Ser Ile Phe Tyr Phe Phe Lys Ile
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 Ala Asn Phe Phe His Pro Leu Phe Leu Trp Ile Lys Trp Arg Ile Asp
 100 105 110
 Lys Leu Ile Leu Arg Thr Leu Leu Ala Cys Leu Ile Leu Ser Leu Cys
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 Phe Ser Leu Pro Val Thr Glu Asn Leu Ala Asp Asp Phe Arg Arg Cys
 130 135 140
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 Lys Ala Gly Tyr Ala Ser Val Lys Val Asn Leu Asn Leu Val Met Leu
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 Phe Pro Phe Ser Val Ser Leu Val Ser Phe Leu Leu Leu Ile Leu Ser
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 Leu Trp Arg His Thr Arg Gln Met Gln Leu Asn Val Thr Gly Tyr Asn
 195 200 205
 Asp Pro Ser Thr Thr Ala His Val Lys Ala Thr Lys Ala Val Ile Ser
 210 215 220
 Phe Leu Val Leu Phe Ile Val Tyr Cys Leu Ala Phe Leu Ile Ala Thr
 225 230 235 240
 Ser Ser Tyr Phe Met Pro Glu Ser Glu Leu Ala Val Ile Trp Gly Glu
 245 250 255
 Leu Ile Ala Leu Ile Tyr Pro Ser Ser His Ser Phe Ile Leu Ile Leu
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 Lys Thr Met Leu Lys Gly Arg Lys Tyr
 290 295

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 <213> Rattus sp.

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 Ala Trp Leu Lys Tyr Met Lys Tyr Ser Phe Ser Tyr Leu Ala Gly Thr
 65 70 75 80
 Glu Leu Arg Val Met Met Leu Thr Trp Val Val Ser Asn His Phe Ser
 85 90 95
 Leu Trp Leu Ala Thr Ile Leu Ser Ile Phe Tyr Leu Leu Lys Ile Ala
 100 105 110
 Ser Phe Ser Arg Pro Val Phe Leu Tyr Leu Lys Trp Arg Val Lys Lys
 115 120 125
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 130 135 140
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 145 150 155 160
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 165 170 175
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 180 185 190
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 210 215 220
 Lys Ala His Val Asn Ala Leu Arg Ile Met Val Ser Phe Leu Leu Leu
 225 230 235 240
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<213> Rattus sp.

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<223> n is a, c, g, or t

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<211> 314
<212> PRT
<213> Rattus sp.

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Trp Asp Trp Val Val Lys Arg Lys Leu Ser Thr Ile Asp Lys Ile Leu
35          40          45
Leu Thr Leu Ala Ile Ser Arg Ile Thr Leu Ile Trp Glu Met Tyr Ala
50          55          60
Cys Phe Lys Ile Val Tyr Gly Ser Ser Ser Phe Ile Phe Gly Met Lys
65          70          75          80
Leu Gln Ile Leu Tyr Phe Ala Trp Ile Leu Ser Ser His Phe Ser Leu
85          90          95
Trp Phe Ala Thr Ala Leu Ser Ile Phe Tyr Leu Leu Arg Ile Ala Asn
100         105         110

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Cys Ser Trp Lys Ile Phe Leu Tyr Leu Lys Trp Arg Leu Lys Gln Val
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 Met Gln Arg Thr Leu Glu Glu Arg Pro Tyr Gln Tyr Gly Gly Asn Thr
 145 150 155 160
 Ser Glu Asp Ser Met Glu Thr Asp Phe Ala Lys Phe Thr Glu Leu Ile
 165 170 175
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 180 185 190
 Ile Ser Phe Leu Leu Leu Ile Phe Ser Leu Trp Lys His Leu Gln Lys
 195 200 205
 Met Gln Leu Ser Ser Arg Gly His Gly Asp Pro Ser Thr Lys Ala His
 210 215 220
 Arg Asn Ala Leu Arg Ile Met Val Ser Phe Leu Leu Leu Tyr Thr Ser
 225 230 235 240
 Tyr Phe Leu Ser Leu Leu Ile Ser Trp Ile Ala Gln Lys His His Ser
 245 250 255
 Lys Leu Val Asp Ile Ile Gly Ile Ile Thr Glu Leu Met Tyr Pro Ser
 260 265 270
 Val His Ser Phe Ile Leu Ile Leu Gly Asn Ser Lys Leu Lys Gln Thr
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<211> 1886

<212> DNA

<213> Rattus sp.

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<223> n is a, c, g, or t

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Asp Leu Arg Ala Thr
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 <212> DNA
 <213> Rattus sp.

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<210> 95

<211> 137

<212> PRT

<213> Rattus sp.

<400> 95

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          20           25           30

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Ala Leu Val Asn Ile Val Asp Trp Ile Lys Arg Arg Arg Ile Ser Ser
 35 40 45

Val Asp Lys Ile Leu Thr Thr Leu Ala Leu Thr Arg Leu Ile Tyr Ala
 50 55 60

Trp Ser Met Leu Ile Phe Ile Leu Leu Phe Ile Leu Gly Pro His Leu
 65 70 75 80

Ile Met Arg Ser Glu Ile Leu Thr Ser Met Gly Val Ile Trp Val Val
 85 90 95

Asn Asn His Phe Ser Ile Trp Leu Ala Thr Cys Leu Gly Val Phe Tyr
 100 105 110

Phe Leu Lys Ile Ala Asn Phe Ser Asn Ser Leu Phe Leu Tyr Leu Lys
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Trp Arg Val Lys Lys Val Val Leu Met
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<210> 96
 <211> 818
 <212> DNA
 <213> Rattus sp.

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 aacatgagga gcttttttaa tgccacttag acattataaa ctgaagcatg ttcttacaca 420
 caataaagca acgtgatatt tttactttga taatcatatt ttttgtggaa ataacaatgg 480
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 aaatacttac atcaatgggt gttatctggg tggatgaaca tcaattcagc atctggcttg 720
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 ttacacataa gtggagagtt aaaaaagtgg ttttaagt 818

<210> 97
 <211> 104
 <212> PRT
 <213> Rattus sp.

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 20 25 30
 Leu Phe Arg Ile Phe Leu Leu Trp Ile Ile Phe Thr Asp Ser Leu Ile
 35 40 45
 Ile Val Phe Ser Tyr His Ala His Asp Ser Gly Ile Arg Met Gln Leu
 50 55 60
 Ile Asp Val Phe Trp Thr Phe Thr Thr His Phe Ser Ile Trp Leu Ile
 65 70 75 80
 Ser Cys Leu Ser Val Phe Tyr Cys Leu Lys Ile Ala Thr Phe Ser His
 85 90 95
 Pro Ser Phe Leu Leu Lys Ser Arg
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<210> 98
 <211> 315
 <212> DNA
 <213> Rattus sp.

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<210> 99
 <211> 308
 <212> PRT
 <213> Rattus sp.

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 20 25 30

Arg Glu Trp Leu Trp Arg Gly Arg Leu Leu Pro Ser Asp Met Ile Leu
 35 40 45
 Leu Ser Leu Gly Thr Ser Arg Phe Cys Gln Gln Cys Val Gly Leu Val
 50 55 60
 Asn Ser Phe Tyr Tyr Ser Leu His Leu Val Glu Tyr Ser Arg Ser Leu
 65 70 75 80
 Ala Arg Gln Leu Ile Ser Leu His Met Asp Phe Leu Asn Ser Ala Thr
 85 90 95
 Phe Trp Phe Gly Thr Trp Leu Ser Val Leu Phe Cys Ile Lys Ile Ala
 100 105 110
 Asn Phe Ser His Pro Ala Phe Leu Trp Leu Lys Trp Arg Phe Pro Ala
 115 120 125
 Leu Val Pro Trp Leu Leu Leu Gly Ser Ile Leu Val Ser Phe Ile Val
 130 135 140
 Thr Leu Met Phe Phe Trp Gly Asn His Thr Val Tyr Gln Ala Phe Leu
 145 150 155 160
 Arg Arg Lys Phe Ser Gly Asn Thr Thr Phe Lys Glu Trp Asn Arg Arg
 165 170 175
 Leu Glu Ile Asp Tyr Phe Met Pro Leu Lys Leu Val Thr Thr Ser Ile
 180 185 190
 Pro Cys Ser Leu Phe Leu Val Ser Ile Leu Leu Leu Ile Asn Ser Leu
 195 200 205
 Arg Arg His Ser Gln Arg Met Gln His Asn Ala His Ser Leu Gln Asp
 210 215 220
 Pro Asn Thr Gln Ala His Ser Arg Ala Leu Lys Ser Leu Ile Ser Phe
 225 230 235 240
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 245 250 255
 Val Val Ile Ser Ser Asp Asn Val Trp Tyr Trp Pro Trp Gln Ile Ile
 260 265 270
 Leu Tyr Leu Cys Met Ser Val His Pro Phe Ile Leu Ile Thr Asn Asn
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 Phe Trp Val Thr
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 <211> 1295
 <212> DNA
 <213> Rattus sp.

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<210> 101
 <211> 332
 <212> PRT
 <213> Rattus sp.

<400> 101

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			20					25					30		
Asn	Val	Phe	Ile	Gly	Leu	Val	Asn	Tyr	Ser	Asp	Trp	Val	Lys	Asn	Lys
		35					40					45			
Lys	Ile	Thr	Phe	Ile	Asn	Phe	Ile	Leu	Ile	Cys	Leu	Ala	Ala	Ser	Arg
	50					55					60				
Ile	Ser	Ser	Val	Leu	Val	Val	Phe	Ile	Asp	Ala	Ile	Ile	Leu	Glu	Leu
65					70					75					80
Thr	Pro	His	Val	Tyr	His	Ser	Tyr	Ser	Arg	Val	Lys	Cys	Ser	Asp	Ile
				85					90					95	
Phe	Trp	Val	Ile	Thr	Asp	Gln	Leu	Ser	Thr	Trp	Leu	Ala	Thr	Cys	Leu
			100					105						110	
Ser	Ile	Phe	Tyr	Leu	Leu	Lys	Ile	Ala	His	Phe	Ser	His	Pro	Leu	Phe
		115					120					125			
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Phe	Ser	Leu	Phe	Ser	Leu	Ile	Val	Tyr	Phe	Leu	Leu	Leu	Glu	Leu	Leu
145					150					155					160
Ser	Ile	Trp	Gly	Asp	Ile	Tyr	Val	Ile	Pro	Lys	Ser	Asn	Leu	Thr	Leu
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Tyr	Ser	Glu	Thr	Ile	Lys	Thr	Leu	Ala	Phe	Gln	Lys	Ile	Ile	Val	Phe
			180					185						190	
Asp	Met	Leu	Tyr	Leu	Val	Pro	Phe	Leu	Val	Ser	Leu	Ala	Ser	Leu	Leu
		195					200					205			
Leu	Leu	Phe	Leu	Ser	Leu	Val	Lys	His	Ser	Gln	Asn	Leu	Asp	Arg	Ile
	210					215					220				
Ser	Thr	Thr	Ser	Glu	Asp	Ser	Arg	Ala	Lys	Ile	His	Lys	Lys	Ala	Met
225					230					235					240
Lys	Met	Leu	Leu	Ser	Phe	Leu	Val	Leu	Phe	Ile	Ile	His	Ile	Phe	Cys
				245					250					255	
Met	Gln	Leu	Ser	Arg	Trp	Leu	Phe	Phe	Leu	Phe	Pro	Asn	Asn	Arg	Ser
			260					265					270		
Thr	Asn	Phe	Leu	Leu	Leu	Thr	Leu	Asn	Ile	Phe	Pro	Leu	Ser	His	Thr
		275					280					285			
Phe	Ile	Ile	Ile	Leu	Gly	Asn	Ser	Lys	Leu	Arg	Gln	Arg	Ala	Met	Arg
	290					295					300				

Val Leu Gln His Leu Lys Ser Gln Leu Gln Glu Leu Ile Leu Ser Leu
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His Arg Leu Ser Arg Val Phe Thr Met Glu Ile Ala
 325 330

<210> 102
 <211> 1287
 <212> DNA
 <213> Rattus sp.

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 gatctgtttg gcagcgtcca gaatcagctc tgtgttggtg gtatttattg atgcaatcat 420
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<210> 103
 <211> 68
 <212> PRT
 <213> Rattus sp.

<400> 103
 Val Ala Asn Ile Met Asp Trp Val Lys Arg Arg Lys Leu Ser Ala Val
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 Asp Gln Leu Leu Thr Val Leu Ala Ile Ser Arg Ile Thr Leu Leu Trp
 20 25 30
 Ser Leu Tyr Ile Leu Lys Ser Thr Phe Ser Met Val Pro Asn Phe Glu
 35 40 45
 Val Ala Ile Pro Ser Thr Arg Leu Thr Asn Leu Val Trp Ile Ile Ser
 50 55 60
 Asn His Phe Asn
 65

<210> 104
 <211> 206
 <212> DNA
 <213> Rattus sp.

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 cattttcaat ggtgccaaac tttgaggtag ctataccgtc aacaagacta actaatcttg 180
 tctggataat ttctaaccat tttaat 206

<210> 105
 <211> 327
 <212> PRT
 <213> Mus musculus

<400> 105
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 20 25 30
 Phe Met Ala Leu Val His Cys Met Asp Trp Val Lys Arg Lys Lys Met
 35 40 45
 Ser Leu Val Asn Lys Ile Leu Thr Ala Leu Ala Ile Ser Arg Ile Phe
 50 55 60
 His Leu Ser Leu Leu Leu Ile Ser Leu Val Ile Phe Phe Ser Tyr Ser
 65 70 75 80

Asp Ile Pro Met Thr Ser Arg Met Thr Gln Val Ser Asn Asn Val Trp
 85 90 95
 Ile Ile Val Asn His Phe Ser Ile Trp Leu Ser Thr Cys Leu Ser Val
 100 105 110
 Leu Tyr Phe Leu Lys Ile Ser Asn Phe Ser Asn Ser Phe Phe Leu Tyr
 115 120 125
 Leu Lys Trp Arg Val Glu Lys Val Val Ser Val Thr Leu Leu Val Ser
 130 135 140
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 145 150 155 160
 Ile Cys Ile Lys Glu Cys Gln Arg Asn Ile Ser Cys Ser Phe Ser Ser
 165 170 175
 His Tyr Tyr Ala Lys Cys His Arg Gln Val Ile Arg Leu His Ile Ile
 180 185 190
 Phe Leu Ser Val Pro Val Val Leu Ser Leu Ser Thr Phe Leu Leu Leu
 195 200 205
 Ile Phe Ser Leu Trp Thr Leu His Gln Arg Met Gln Gln His Val Gln
 210 215 220
 Gly Gly Arg Asp Ala Arg Thr Thr Ala His Phe Lys Ala Leu Gln Thr
 225 230 235 240
 Val Ile Ala Phe Phe Leu Leu Tyr Ser Ile Phe Ile Leu Ser Val Leu
 245 250 255
 Ile Gln Asn Glu Leu Leu Lys Lys Asn Leu Phe Val Val Phe Cys Glu
 260 265 270
 Val Val Tyr Ile Ala Phe Pro Thr Phe His Ser Tyr Ile Leu Ile Val
 275 280 285
 Gly Asp Met Lys Leu Arg Gln Ala Cys Leu Pro Leu Cys Ile Ile Ala
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 Ala Glu Ile Gln Thr Thr Leu Cys Arg Asn Phe Arg Ser Leu Lys Tyr
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 Phe Arg Leu Cys Cys Ile Phe
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<210> 106

<211> 1374

<212> DNA

<213> Mus musculus

<400> 106

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<210> 107

<211> 327

<212> PRT

<213> Mus musculus

<400> 107

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Phe Ile Phe Gly Asn Leu Ser Asn Gly Phe Ile Val Leu Ser Asn Phe
20           25           30

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Leu Asp Trp Val Ile Lys Gln Lys Leu Ser Leu Ile Asp Lys Ile Leu
35           40           45

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Leu	Thr	Leu	Ala	Ile	Ser	Arg	Ile	Thr	Leu	Ile	Trp	Glu	Ile	Tyr	Ala	50	55	60	
Trp	Phe	Lys	Ser	Leu	Tyr	Asp	Pro	Ser	Ser	Phe	Leu	Ile	Gly	Ile	Glu	65	70	75	80
Phe	Gln	Ile	Ile	Tyr	Phe	Ser	Trp	Val	Leu	Ser	Ser	His	Phe	Ser	Leu	85	90	95	
Trp	Leu	Ala	Thr	Thr	Leu	Ser	Val	Phe	Tyr	Leu	Leu	Arg	Ile	Ala	Asn	100	105	110	
Cys	Ser	Trp	Gln	Ile	Phe	Leu	Tyr	Leu	Lys	Trp	Arg	Leu	Lys	Gln	Leu	115	120	125	
Ile	Val	Gly	Met	Leu	Leu	Gly	Ser	Leu	Val	Phe	Leu	Leu	Gly	Asn	Leu	130	135	140	
Met	Gln	Ser	Met	Leu	Glu	Glu	Arg	Phe	Tyr	Gln	Tyr	Gly	Arg	Asn	Thr	145	150	155	160
Ser	Val	Asn	Thr	Met	Ser	Asn	Asp	Leu	Ala	Met	Trp	Thr	Glu	Leu	Ile	165	170	175	
Phe	Phe	Asn	Met	Ala	Met	Phe	Ser	Val	Ile	Pro	Phe	Thr	Leu	Ala	Leu	180	185	190	
Ile	Ser	Phe	Leu	Leu	Leu	Ile	Phe	Ser	Leu	Trp	Lys	His	Leu	Gln	Lys	195	200	205	
Met	Gln	Leu	Ile	Ser	Arg	Arg	His	Arg	Asp	Pro	Ser	Thr	Lys	Ala	His	210	215	220	
Met	Asn	Ala	Leu	Arg	Ile	Met	Val	Ser	Phe	Leu	Leu	Leu	Tyr	Thr	Met	225	230	235	240
His	Phe	Leu	Ser	Leu	Leu	Ile	Ser	Trp	Ile	Ala	Gln	Lys	His	Gln	Ser	245	250	255	
Glu	Leu	Ala	Asp	Ile	Ile	Gly	Met	Ile	Thr	Glu	Leu	Met	Tyr	Pro	Ser	260	265	270	
Val	His	Ser	Cys	Ile	Leu	Ile	Leu	Gly	Asn	Ser	Lys	Leu	Lys	Gln	Thr	275	280	285	
Ser	Leu	Cys	Met	Leu	Arg	His	Leu	Arg	Cys	Arg	Leu	Lys	Gly	Glu	Asn	290	295	300	
Ile	Thr	Ile	Ala	Tyr	Ser	Asn	Gln	Ile	Thr	Ser	Phe	Cys	Val	Phe	Cys	305	310	315	320
Val	Ala	Asn	Lys	Ser	Met	Arg										325			

<210> 108

<211> 1759

<212> DNA

<213> Mus musculus

<400> 108

cagcacagtg aaaaactcat gggccacttg gtcacccagg gacaggcgac gctgttatat	60
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gtggagttta tttttgggaa tttgagcaat ggattcatag tgttgtcaaa cttcttggac	180
tgggtcatta aacaaaagct ttccttaata gataaaattc ttcttacatt ggcaatttca	240
agaatcactc tcatctggga aatatatgct tggtttaaaa gtttatatga tccatcttcc	300
tttttaattg gaatagaatt tcaaattatt tatttttagct gggtccttcc tagtcacttc	360
agcctctggc ttgccacaac tctcagcgtc ttttatttac tcagaatagc taactgctcc	420
tggcagatct ttctctattt gaaatggaga cttaaacaac tgatttgtgg gatgttgctg	480
ggaagcttgg tgttcttgtc tggaaatctg atgcaaagca tgcttgaaga gaggttctat	540
caatatggaa ggaacacaag tgtgaatacc atgagcaatg accttgcaat gtggaccgag	600
ctgatctttt tcaacatggc tatgttctct gtaataccat ttacattggc cttgatttct	660
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cagagtgaac tggctgatat tattggtatg ataactgaac tcatgtatcc ttcagtccat	900
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catttgagat gtaggctgaa aggagagaat atcacaattg catatagcaa ccaaataact	1020
agcttttgtg tattctgtgt tgcaaacaaa tctatgaggt agttgttcaa ggaatccttc	1080
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caaggtttgt atacactagt ggggctggga caccaaccca agcacaaaac ctagctataa	1200
cctatcctgg ctgcaggata tgctggaaca atggtggcct ggaaattgtg ggactggcaa	1260
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tggaaaaaga aagactcgtg ttaatgatct atcaaatatt tcctaataatg attctgataa	1440
actcatatat tagtccctgt cctaatactc atcactggga ctccctccca gcacctgatg	1500
ggagcagata gagatctaca tccaaatagt aagtgtatct tggggaactc cacttaagaa	1560

tagaaggaac aattatgaga gccagagtga tccagaacac taggatcaca gaatcaacta 1620
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 aacaatggat aaggaattc 1759

<210> 109
 <211> 312
 <212> PRT
 <213> Mus musculus

<400> 109
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 Ile Ser Leu Glu Phe Ile Ile Gly Ile Leu Gly Asn Val Phe Ile Ala
 20 25 30
 Leu Val Asn Ile Ile Asp Trp Val Lys Arg Gly Lys Ile Ser Ala Val
 35 40 45
 Asp Lys Thr Tyr Met Ala Leu Ala Ile Ser Arg Thr Ala Phe Leu Leu
 50 55 60
 Ser Leu Ile Thr Gly Phe Leu Val Ser Leu Leu Asp Pro Ala Leu Leu
 65 70 75 80
 Gly Met Arg Thr Met Val Arg Leu Leu Thr Ile Ser Trp Met Val Thr
 85 90 95
 Asn His Phe Ser Val Trp Phe Ala Thr Cys Leu Ser Ile Phe Tyr Phe
 100 105 110
 Leu Lys Ile Ala Asn Phe Ser Asn Ser Ile Phe Leu Val Leu Lys Trp
 115 120 125
 Glu Ala Lys Lys Val Val Ser Val Thr Leu Val Val Ser Val Ile Ile
 130 135 140
 Leu Ile Met Asn Ile Ile Val Ile Asn Lys Phe Thr Asp Arg Leu Gln
 145 150 155 160
 Val Asn Thr Leu Gln Asn Cys Ser Thr Ser Asn Thr Leu Lys Asp Tyr
 165 170 175
 Gly Leu Phe Leu Phe Ile Ser Thr Gly Phe Thr Leu Thr Pro Phe Ala
 180 185 190
 Val Ser Leu Thr Met Phe Leu Leu Leu Ile Phe Ser Leu Trp Arg His
 195 200 205
 Leu Lys Asn Met Cys His Ser Ala Thr Gly Ser Arg Asp Val Ser Thr
 210 215 220

Val Ala His Ile Lys Gly Leu Gln Thr Val Val Thr Phe Leu Leu Leu
 225 230 235 240

Tyr Thr Ala Phe Val Met Ser Leu Leu Ser Glu Ser Leu Asn Ile Asn
 245 250 255

Ile Gln His Thr Asn Leu Leu Ser His Phe Leu Arg Ser Ile Gly Val
 260 265 270

Ala Phe Pro Thr Gly His Ser Cys Val Leu Ile Leu Gly Asn Ser Lys
 275 280 285

Leu Arg Gln Ala Ser Leu Ser Val Ile Leu Trp Leu Arg Tyr Lys Tyr
 290 295 300

Lys His Ile Glu Asn Trp Gly Pro
 305 310

<210> 110

<211> 1484

<212> DNA

<213> Mus musculus

<400> 110

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caattttttg tgtatgtgtg gagaacataa accatttcat tagtgaaatt tggcttttgg 180

gtgacattgt ctatgatagt tctgaaagtg attatgttaa gaatcagaca cagccgtcta 240

gaagattgta ttaacacatc tttggtagtt cagaagaaat tagatcatca tgggtgtgac 300

aataagggct attttatggg taacattgat aactattata agtctggagt ttatcatagg 360

aatttttagga aatgtattca tagctctcgt gaacatcata gactgggtta aaagaggaaa 420

gatctctgca gtggataaga cctatatggc cctggccatc tccaggactg cttttttatt 480

gtcactaatc acaggggttct tgggtatcatt attggacca gctttatttg gaatgagaac 540

gatggtaagg ctccctacta tttcctggat ggtgaccaat catttcagtg tctggtttgc 600

aacatgcctc agtatctttt attttctcaa gatagctaatt ttctcaaatt ctattttcct 660

tgttctcaaa tgggaagcta aaaaagtggt atcagtgaca ttgggtggtat ctgtgataat 720

cttgatcatg aacattatag tcataaacia attcactgac agacttcaag taaacacact 780

ccagaactgt agtacaagta acactttaaa agattatggg ctctttttat tcattagcac 840

tgggtttaca ctcaccccat tcgctgtgtc tttgacaatg tttcttctgc tcattctctc 900

cctgtggaga catctgaaga atatgtgtca cagtgccaca ggctccagag atgtcagcac 960

agtggccac ataaaaggct tgcaaaactgt ggtaaccttc ctgttactat atactgcttt 1020

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tggtatgtca cttcttttcag agtcttttgaa tattaacatt caacatacaa atcttctttc 1080
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tggaacacgt aagctgaggc aagcctctct ttctgtgata ttgtggctga ggtataagta 1200
caaacatata gagaattggg gcccttaa atcatcaggg atccttttcc acattctaga 1260
aaaaaatcag ttaataagaa caggaattta ggaaggaatc tgaaattatg aatctcatag 1320
gccatgaacc ttcagacaaa ggattcatta gagagataga gagagaacat tggtatctgt 1380
aactggacag gcaacactgt agattatgaa aataaatgtc agtctgtaat ggaaagcaaa 1440
acatgctata ttttattaat tgggttttggg ttaaggtcgg gata 1484

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<210> 111
<211> 302
<212> PRT
<213> Mus musculus

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<400> 111
Met Leu Ser Ala Leu Glu Ser Ile Leu Leu Ser Val Ala Thr Ser Glu
1          5          10          15

Ala Met Leu Gly Val Leu Gly Asn Thr Phe Ile Val Leu Val Asn Tyr
20          25          30

Thr Asp Trp Val Arg Asn Lys Lys Leu Ser Lys Ile Asn Phe Ile Leu
35          40          45

Thr Gly Leu Ala Ile Ser Arg Ile Phe Thr Ile Trp Ile Ile Thr Leu
50          55          60

Asp Ala Tyr Thr Lys Val Phe Leu Leu Thr Met Leu Met Pro Ser Ser
65          70          75          80

Leu His Glu Cys Met Ser Tyr Ile Trp Val Ile Ile Asn His Leu Ser
85          90          95

Val Trp Phe Ser Thr Ser Leu Gly Ile Phe Tyr Phe Leu Lys Ile Ala
100         105         110

Asn Phe Ser His Tyr Ile Phe Leu Trp Met Lys Arg Arg Ala Asp Lys
115         120         125

Val Phe Val Phe Leu Ile Val Phe Leu Ile Ile Thr Trp Leu Ala Ser
130         135         140

Phe Pro Leu Ala Val Lys Val Ile Lys Asp Val Lys Ile Tyr Gln Ser
145         150         155         160

Asn Thr Ser Trp Leu Ile His Leu Glu Lys Ser Glu Leu Leu Ile Asn
165         170         175

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Tyr Val Phe Ala Asn Met Gly Pro Ile Ser Leu Phe Ile Val Ala Ile
 180 185 190
 Ile Ala Cys Phe Leu Leu Thr Ile Ser Leu Trp Arg His Ser Arg Gln
 195 200 205
 Met Gln Ser Ile Gly Ser Gly Phe Arg Asp Leu Asn Thr Glu Ala His
 210 215 220
 Met Lys Ala Met Lys Val Leu Ile Ala Phe Ile Ile Leu Phe Ile Leu
 225 230 235 240
 Tyr Phe Leu Gly Ile Leu Ile Glu Thr Leu Cys Leu Phe Leu Thr Asn
 245 250 255
 Asn Lys Leu Leu Phe Ile Phe Gly Phe Thr Leu Ser Ala Met Tyr Pro
 260 265 270
 Cys Cys His Ser Phe Ile Leu Ile Leu Thr Ser Arg Glu Leu Lys Gln
 275 280 285
 Asp Thr Met Arg Ala Leu Gln Arg Leu Lys Cys Cys Glu Thr
 290 295 300

<210> 112

<211> 1529

<212> DNA

<213> Mus musculus

<400> 112

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tgagtgcact ggaaagcatc ctcctttctg ttgccactag tgaagccatg ctgggagttt	120
tagggaacac atttattgta cttgtaaact acacagactg ggtcaggaat aagaaactct	180
ctaagattaa ctttattctc actggcttag caatttccag gatttttaacc atatggataa	240
taactttaga tgcataatac aagggttttcc ttctgactat gcttatgccg agcagtctac	300
atgaatgcat gagttacata tgggtaatta ttaaccatct gagcgtttgg tttagcacca	360
gcctcggcat cttttatctt ctgaagatag caaatttttc ccactacata tttctctgga	420
tgaagagaag agctgataaa gtttttgtct ttctaattgt attcttaatt ataacgtggc	480
tagcttcctt tccgctagct gtgaaggcca ttaaagatgt taaaatatat cagagcaaca	540
catcctggct gatccacctg gagaagagtg agttacttat aaactatggt tttgccataa	600
tggggcccat ttccctcttt attgtagcca taattgcttg tttcttggtt accatttccc	660
tttgagagaca cagcaggcag atgcaatcca ttggatcagg attcagagat ctcaacacag	720
aagctcacat gaaagccatg aaagttttta ttgcatttat catcctcttt atcttatatt	780
ttttgggtat tctcatagaa acattatgct tgtttcttac aaacaataaa cttctcttta	840

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tttttggctt cactttgtca gccatgtatc cctggttgcca ttccctttatc ctaattctaa    900
caagcagggg gctgaagcaa gccactatga gggcactgca gagattaaaa tgctgtgaga    960
cttgacagag aatgaatgt tctggcacag ttcagcaggg aatccctgga gccctttcca    1020
ttcccactat gttctcacac tgtctttagt tgaattgtta aaagtttttg aaacctttgg    1080
caactgattg actgcagcta cgccagtgtg agattttcat agtaagagca aacattgaaa    1140
ataagacttc tcagtcttat ttcattgagt ttctaaagca ttgacacca ttcaccagaa    1200
aaaccaaagg ggaagagagg agttttcaga catgtgtgat gaatcttgat atttaggaca    1260
tggaattgag gagccagagg gatgctaccg tgtgtctaca gctttgtttg ttaaatagct    1320
acttttcctt tccagtttag ttaaagtaga tgcttggagt agtggtgaaa atcatggcag    1380
tagatgggat ctgtgggaag tggttgagga agcaggctgt ttctgaacga agagaccaga    1440
ggactgattg aactgggtcat tgtgtatatc aaaaatagtg atttcagatg aagccaagtt    1500
gtagagcaaa gatatctgag gaagaattc    1529

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<210> 113

<211> 300

<212> PRT

<213> Mus musculus

<400> 113

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Met Leu Ser Ala Ala Glu Gly Ile Leu Leu Ser Ile Ala Thr Val Glu
1          5          10          15
Ala Gly Leu Gly Val Leu Gly Asn Thr Phe Ile Ala Leu Val Asn Cys
20          25          30
Met Asp Trp Ala Lys Asn Asn Lys Leu Ser Met Thr Gly Phe Leu Leu
35          40          45
Ile Gly Leu Ala Thr Ser Arg Ile Phe Ile Val Trp Leu Leu Thr Leu
50          55          60
Asp Ala Tyr Ala Lys Leu Phe Tyr Pro Ser Lys Tyr Phe Ser Ser Ser
65          70          75          80
Leu Ile Glu Ile Ile Ser Tyr Ile Trp Met Thr Val Asn His Leu Thr
85          90          95
Val Trp Phe Ala Thr Ser Leu Ser Ile Phe Tyr Phe Leu Lys Ile Ala
100         105         110
Asn Phe Ser Asp Cys Val Phe Leu Trp Leu Lys Arg Arg Thr Asp Lys
115         120         125
Ala Phe Val Phe Leu Leu Gly Cys Leu Leu Thr Ser Trp Val Ile Ser
130         135         140

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Phe Ser Phe Val Val Lys Val Met Lys Asp Gly Lys Val Asn His Arg
 145 150 155 160
 Asn Arg Thr Ser Glu Met Tyr Trp Glu Lys Arg Gln Phe Thr Ile Asn
 165 170 175
 Tyr Val Phe Leu Asn Ile Gly Val Ile Ser Leu Phe Met Met Thr Leu
 180 185 190
 Thr Ala Cys Phe Leu Leu Ile Met Ser Leu Trp Arg His Ser Arg Gln
 195 200 205
 Met Gln Ser Gly Val Ser Gly Phe Arg Asp Leu Asn Thr Glu Ala His
 210 215 220
 Val Lys Ala Ile Lys Phe Leu Ile Ser Phe Ile Ile Leu Phe Val Leu
 225 230 235 240
 Tyr Phe Ile Gly Val Ser Ile Glu Ile Ile Cys Ile Phe Ile Pro Glu
 245 250 255
 Asn Lys Leu Leu Phe Ile Phe Gly Phe Thr Thr Ala Ser Ile Tyr Pro
 260 265 270
 Cys Cys His Ser Phe Ile Leu Ile Leu Ser Asn Ser Gln Leu Lys Gln
 275 280 285
 Ala Phe Val Lys Val Leu Gln Gly Leu Lys Phe Phe
 290 295 300

<210> 114

<211> 903

<212> DNA

<213> Mus musculus

<400> 114

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gttttaggga acacatttat tgcactggta aactgcatgg actgggcca gaacaataag	120
ctttctatga ctggcttctt tctcatcggc ttagcaactt ccaggatttt tattgtgtgg	180
ctattaactt tagatgcata tgcaaagcta ttctatccaa gtaagtattt ttctagtagt	240
ctgattgaaa tcatctotta tatatggatg actgtgaatc acctgactgt ctggtttgcc	300
accagcctaa gcatcttcta tttcctgaag atagccaatt tttccgactg tgtatttctc	360
tgggtgaaga ggagaactga taaagctttt gtttttctct tggggtgttt gctaacttca	420
tgggtaatct ccttctcatt tgttgtgaag gtgatgaagg acggtaaagt gaatcataga	480
aacaggacct cggagatgta ctgggagaaa aggcaattca ctattaacta cgttttcctc	540
aatattggag tcatttctct ctttatgatg accttaactg catgtttctt gttaattatg	600


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tcactttgga gacacagcag gcagatgcag tctgggtgtt caggattcag agacctcaac 660
acagaagctc atgtgaaagc cataaaattt ttaatttcat ttatcatcct tttcgtcttg 720
tattttatag gtgttttcaat agaaattatc tgcattttta taccagaaaa caaactgcta 780
tttatttttg gtttcacaac tgcattccata tatccttgct gtcactcatt tattctaatt 840
ctatctaaca gccagctaaa gcaagccttt gtaaaggtag tgcaaggatt aaagttcttt 900
tag 903

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<210> 115

<211> 308

<212> PRT

<213> Mus musculus

<400> 115

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Met Leu Thr Val Ala Glu Gly Ile Leu Leu Cys Phe Val Thr Ser Gly
1          5          10          15

Ser Val Leu Gly Val Leu Gly Asn Gly Phe Ile Leu His Ala Asn Tyr
          20          25          30

Ile Asn Cys Val Arg Lys Lys Phe Ser Thr Ala Gly Phe Ile Leu Thr
          35          40          45

Gly Leu Ala Ile Cys Arg Ile Phe Val Ile Cys Ile Ile Ile Ser Asp
          50          55          60

Gly Tyr Leu Lys Leu Phe Ser Pro His Met Val Ala Ser Asp Ala His
65          70          75          80

Ile Ile Val Ile Ser Tyr Ile Trp Val Ile Ile Asn His Thr Ser Ile
          85          90          95

Trp Phe Ala Thr Ser Leu Asn Leu Phe Tyr Leu Leu Lys Ile Ala Asn
          100          105          110

Phe Ser His Tyr Ile Phe Phe Cys Leu Lys Arg Arg Ile Asn`Thr Val
          115          120          125

Phe Ile Phe Leu Leu Gly Cys Leu Phe Ile Ser Trp Ser Ile Ala Phe
          130          135          140

Pro Gln Thr Val Lys Ile Phe Asn Val Lys Lys Gln His Arg Asn Val
145          150          155          160

Ser Trp Gln Val Tyr Leu Tyr Lys Asn Glu Phe Ile Val Ser His Ile
          165          170          175

Leu Leu Asn Leu Gly Val Ile Phe Phe Phe Met Val Ala Ile Ile Thr
          180          185          190

Cys Phe Leu Leu Ile Ile Ser Leu Trp Lys His Asn Arg Lys Met Gln
          195          200          205

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Leu Tyr Ala Ser Arg Phe Lys Ser Leu Asn Thr Glu Val His Val Lys
 210 215 220
 Val Met Lys Val Leu Ile Ser Phe Ile Ile Leu Leu Ile Leu His Phe
 225 230 235 240
 Ile Gly Ile Leu Ile Glu Thr Leu Ser Phe Leu Lys Tyr Glu Asn Lys
 245 250 255
 Leu Leu Leu Ile Leu Gly Leu Ile Ile Ser Cys Met Tyr Pro Cys Cys
 260 265 270
 His Ser Phe Ile Leu Ile Leu Ala Asn Ser Gln Leu Lys Gln Ala Ser
 275 280 285
 Leu Lys Ala Leu Lys Gln Leu Lys Cys His Lys Lys Asp Lys Asp Val
 290 295 300
 Arg Val Thr Trp
 305

<210> 116

<211> 1242

<212> DNA

<213> Mus musculus

<400> 116

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tgcatgcaaa ctacattaac tgtgtcagaa agaagtctc cacagctggc tttattctca	180
caggcttggc tatttgcaaga atctttgtca tatgtataat aatctctgat ggatatttaa	240
aattgttttc tccacatatg gttgcctctg atgccacat tatagtgatt tcttacatat	300
gggtaattat caatcataca agtatatggg ttgccaccag cctcaacctc ttctatctcc	360
tgaagatagc aaatttttct cactacatct tcttctgctt gaagagaaga atcaatacag	420
tatttatctt tctcctggga tgcttattta tatcatgggc aattgctttc ccacaaacag	480
tgaagatatt taatgttaaa aagcagcaca gaaatgtttc ctggcagggt tacctctata	540
agaatgaggt cattgtaagc cacattcttc tcaacctggg agttatatcc ttctttatgg	600
tggtatcat tacatgcttc ctattaatta tttcactttg gaaacataac agaaagatgc	660
agttgtatgc ctcaagattc aaaagcctta acacagaagt acatgtgaaa gtcatgaaag	720
ttttaatttc ttttattatc ctgttaatct tgcatttcat agggattttg atagaaacat	780
tgagcttttt aaaatatgaa aataaactgc tacttatttt gggtttgata atttcatgca	840
tgtatccttg ctgtcattca tttatcctaa ttctagcaaa cagtcagctg aagcaggctt	900

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ctttgaaggc actgaagcaa ttaaaatgcc ataagaaaga caaggacgtc agagtgcacat   960
ggtagactta tggagaaatg aatggtcaca agaaatagcc tgggtgtggag atgttgatat   1020
ctctaaagac cgtttcactt ccaaattctt gcaattatctt aaaaaaaaaa gtcttgctga   1080
tatcatggaa tcatgggaaa tgttgcaatt gtgttttggg gacaggggtga ccagtgaagg   1140
tatggttaag cagcgaaaca ctcatacagc tcgttcgttc tttttgtatt ttattttgtg   1200
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<210> 117

<211> 308

<212> PRT

<213> Mus musculus

<400> 117

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Met Leu Asn Ser Ala Glu Gly Ile Leu Leu Cys Val Val Thr Ser Glu
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Ala Val Leu Gly Val Leu Gly Asp Thr Tyr Ile Ala Leu Phe Asn Cys
          20          25          30

Met Asp Tyr Ala Lys Asn Lys Lys Leu Ser Lys Ile Gly Phe Ile Leu
          35          40          45

Ile Gly Leu Ala Ile Ser Arg Ile Gly Val Val Trp Ile Ile Ile Leu
          50          55          60

Gln Gly Tyr Ile Gln Val Phe Phe Pro His Met Leu Thr Ser Gly Asn
65          70          75          80

Ile Thr Glu Tyr Ile Thr Tyr Ile Trp Val Phe Leu Asn His Leu Ser
          85          90          95

Val Trp Phe Val Thr Asn Leu Asn Ile Leu Tyr Phe Leu Lys Ile Ala
          100          105          110

Asn Phe Ser Asn Ser Val Phe Leu Trp Leu Lys Arg Arg Val Asn Ala
          115          120          125

Val Phe Ile Phe Leu Ser Gly Cys Leu Leu Thr Ser Trp Leu Leu Cys
          130          135          140

Phe Pro Gln Met Thr Lys Ile Leu Gln Asn Ser Lys Met His Gln Arg
145          150          155          160

Asn Thr Ser Trp Val His Gln Arg Lys Asn Tyr Phe Leu Ile Asn Gln
          165          170          175

Ser Val Thr Asn Leu Gly Ile Phe Phe Phe Ile Ile Val Ser Leu Ile
          180          185          190

Thr Cys Phe Leu Leu Ile Val Phe Leu Trp Arg His Val Arg Gln Met
          195          200          205

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His Ser Asp Val Ser Gly Phe Arg Asp His Ser Thr Lys Val His Val
 210 215 220
 Lys Ala Met Lys Phe Leu Ile Ser Phe Met Val Phe Phe Ile Leu His
 225 230 235 240
 Phe Val Gly Leu Ser Ile Glu Val Leu Cys Phe Ile Leu Pro Gln Asn
 245 250 255
 Lys Leu Leu Phe Ile Thr Gly Leu Thr Ala Thr Cys Leu Tyr Pro Cys
 260 265 270
 Gly His Ser Ile Ile Val Ile Leu Gly Asn Lys Gln Leu Lys Gln Ala
 275 280 285
 Ser Leu Lys Ala Leu Gln Gln Leu Lys Cys Cys Glu Thr Lys Gly Asn
 290 295 300
 Phe Arg Val Lys
 305

<210> 118

<211> 1754

<212> DNA

<213> Mus musculus

<400> 118

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tgaaatagaa gcttctatct gcttattaac aaactgcaag caaacattag tctgcacaca	180
ttttatagac aagctaaatc ttcaaaagca ataaaaaaga gcaccataa agttctgact	240
ctatcacatg acaataggct tgaaaagatt gtctatgtag ataaagaaga tggcataact	300
tctccatcaa gaagccagta tatgggacat tctccagcag ataatttaca atagatgcag	360
cagaagtaac cttagagatc tgtaaagatg ctgaattcag cagaaggcat cctcctttgt	420
gttgctacta gtgaggctgt gctcggagtt ttaggggaca catatatatgc actttttaac	480
tgcatggact atgctaagaa caagaagctc tctaagatcg gtttcattct cattggcttg	540
gcgatttcca gaattgggtg tgtatggata ataattttac aagggtatat acaagtattt	600
ttccacaca tgcttacctc tggaaacata actgaatata ttacttacat atgggtattt	660
ctcaatcact taagtgtctg gtttgtcacc aacctcaaca tcctctactt tctaaagata	720
gctaattttt ccaactctgt atttctctgg ctgaaaagga gagtcaatgc agtttttatc	780
tttctgtcag gatgcttact tacctcatgg ttactatggt ttccacaaat gacaaagata	840
cttcaaaata gtaaaatgca ccagagaaac acatcttggg tccaccagcg gaaaaattac	900

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tttcttatta accaaagtgt gaccaatctg ggaatctttt tcttcattat tgtatccctg    960
attacctgct ttctgttgat tgttttcctc tggagacatg tcagacaaat gcactcagat    1020
gtttcaggat tcagagacca cagcacaaaa gtacatgtga aagctatgaa atttctaata    1080
tcttttatgg tcttctttat tctgcatttt gtaggccttt ccatagaagt gctatgcttt    1140
attctgccac aaaataaact gctctttata actggtttga cagccacatg cctctatccc    1200
tgcggtcact caatcatcgt aatttttagga aataagcagt taaagcaagc ctctttgaag    1260
gcactgcagc aactaaaatg ctgtgagaca aaaggaaatt tcagagtcaa ataaatgggt    1320
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gtccacgtga agcctcactt catactgtga cttgactatg caaattcttt ccacaaaata    1500
accagataac attcagcctg gagataaatt catttaaagg cttttatggt gaggataaac    1560
aaaaaaaaaa aatcattttt ctgtgattca ctgtaactcc caggatgagt aaaagaaaac    1620
aagacaaatg gttgtgatca gcctttgtgt gtctagacag agctagggac cagatgttga    1680
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<210> 119

<211> 297

<212> PRT

<213> Mus musculus

<400> 119

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Met Leu Trp Glu Leu Tyr Val Phe Val Phe Ala Ala Ser Val Phe Leu
1           5           10          15

Asn Phe Val Gly Ile Ile Ala Asn Leu Phe Ile Ile Val Ile Ile Ile
20          25          30

Lys Thr Trp Val Asn Ser Arg Arg Ile Ala Ser Pro Asp Arg Ile Leu
35          40          45

Phe Ser Leu Ala Ile Thr Arg Phe Leu Thr Leu Gly Leu Phe Leu Leu
50          55          60

Asn Ser Val Tyr Ile Ala Thr Asn Thr Gly Arg Ser Val Tyr Phe Ser
65          70          75          80

Thr Phe Phe Leu Leu Cys Trp Lys Phe Leu Asp Ala Asn Ser Leu Trp
85          90          95

Leu Val Thr Ile Leu Asn Ser Leu Tyr Cys Val Lys Ile Thr Asn Phe
100         105         110

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Gln His Pro Val Phe Leu Leu Leu Lys Arg Thr Ile Ser Met Lys Thr
 115 120 125
 Thr Ser Leu Leu Leu Ala Cys Leu Leu Ile Ser Ala Leu Thr Thr Leu
 130 135 140
 Leu Tyr Tyr Met Leu Ser Gln Ile Ser Arg Phe Pro Glu His Ile Ile
 145 150 155 160
 Gly Arg Asn Asp Thr Ser Phe Asp Leu Ser Asp Gly Ile Leu Thr Leu
 165 170 175
 Val Ala Ser Leu Val Leu Asn Ser Leu Leu Gln Phe Met Leu Asn Val
 180 185 190
 Thr Phe Ala Ser Leu Leu Ile His Ser Leu Arg Arg His Ile Gln Lys
 195 200 205
 Met Gln Arg Asn Arg Thr Ser Phe Trp Asn Pro Gln Thr Glu Ala His
 210 215 220
 Met Gly Ala Met Arg Leu Met Ile Cys Phe Leu Val Leu Tyr Ile Pro
 225 230 235 240
 Tyr Ser Ile Ala Thr Leu Leu Tyr Leu Pro Ser Tyr Met Arg Lys Asn
 245 250 255
 Leu Arg Ala Gln Ala Ile Cys Met Ile Ile Thr Ala Ala Tyr Pro Pro
 260 265 270
 Gly His Ser Val Leu Leu Ile Ile Thr His His Lys Leu Lys Ala Lys
 275 280 285
 Ala Lys Lys Ile Phe Cys Phe Tyr Lys
 290 295

<210> 120

<211> 1475

<212> DNA

<213> Mus musculus

<400> 120

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tttgccatgc tggaaaataa aaaggagacc tctttccagg ctgcatcctg tgtctgctta      180
cttattttcag tttgttttca tcggcaccaa acgaggaaag atgctctggg aactgtatgt      240
atgtgtgttt gctgcctcgg tttttttaaa ttttgtagga atcattgcaa atctatttat      300
tatagtgata attattaaga cttgggtcaa cagtcgcaga attgcctctc cggataggat      360
cctgttcagc ttggccatca ctagattcct gactttgggg ttgtttctac tgaacagtgt      420
ctacattgct acaaatactg gaaggtcagt ctacttttcc acattttttc tattgtgttg      480

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gaagtttctg gatgcaaaca gtctctgggt agtgaccatt ctgaacagct tgtattgtgt 540
gaagattact aattttcaac acccagtgtt tctcctgttg aaacggacta tctctatgaa 600
gaccaccagc ctgctgttgg cctgtcttct gatttcagcc ctcaccactc tcctatatta 660
tatgctctca cagatatcac gttttcctga acacataatt gggagaaatg acacgtcatt 720
tgacctcagt gatggtatct tgacgttagt agcctctttg gtcttgaact cacttctaca 780
gtttatgctc aatgtgactt ttgcttcctt gttaatacat tccttgagaa gacatatata 840
gaagatgcag agaaacagga ccagcttttg gaatccccag acggagggtc acatgggtgc 900
tatgaggctg atgatctggt tcctcgtgct ctacattcca tattcaattg ctaccctgct 960
ctatcttcct tcctatatga ggaagaatct gagagcccag gccatttgca tgattattac 1020
tgctgcttac cctccaggac attctgtcct cctcattatc acacatcata aactgaaagc 1080
taaagcaaag aagattttct gtttctacaa gtagcagaat ttcattagta gttaacagca 1140
tcaattcatg gtttggttgc attagaaatg tctcagtgat ctaaggactt aattttgtga 1200
tcttgtatct ggcacctga ccctgagact aagtgttat attttggcca atacagcatc 1260
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atttttcatg gctatcacat tcctagacaa tggaaatcac catactgttt cgctagctac 1380
tgaagtacca ggggaaagtc catgaatgaa ggccacattg tgatgttctt ggtagcaca 1440
gattagagaa tttggcctca actgagcaag atatc 1475

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<210> 121
<211> 316
<212> PRT
<213> Mus musculus

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<400> 121
Met Glu His Leu Leu Lys Arg Thr Phe Asp Ile Thr Glu Asn Ile Leu
1          5          10          15
Leu Ile Ile Leu Phe Ile Glu Leu Ile Ile Gly Leu Ile Gly Asn Gly
20          25          30
Phe Thr Ala Leu Val His Cys Met Asp Trp Val Lys Arg Lys Lys Met
35          40          45
Ser Leu Val Asn Lys Ile Leu Thr Ala Leu Ala Thr Ser Arg Ile Phe
50          55          60
Leu Leu Trp Phe Met Leu Val Gly Phe Pro Ile Ser Ser Leu Tyr Pro
65          70          75          80

```

Tyr Leu Val Thr Thr Arg Leu Met Ile Gln Phe Thr Ser Thr Leu Trp
 85 90 95
 Thr Ile Ala Asn His Ile Ser Val Trp Phe Ala Thr Cys Leu Ser Val
 100 105 110
 Phe Tyr Phe Leu Lys Ile Ala Asn Phe Ser Asn Ser Pro Phe Leu Tyr
 115 120 125
 Leu Lys Arg Arg Val Glu Lys Val Val Ser Val Thr Leu Leu Val Ser
 130 135 140
 Leu Val Leu Leu Phe Leu Asn Ile Leu Leu Leu Asn Leu Glu Ile Asn
 145 150 155 160
 Met Cys Ile Asn Glu Tyr His Gln Ile Asn Ile Ser Tyr Ile Phe Ile
 165 170 175
 Ser Tyr Tyr His Leu Ser Cys Gln Ile Gln Val Leu Gly Ser His Ile
 180 185 190
 Ile Phe Leu Ser Val Pro Val Val Leu Ser Leu Ser Thr Phe Leu Leu
 195 200 205
 Leu Ile Phe Ser Leu Trp Thr Leu His Lys Arg Met Gln Gln His Val
 210 215 220
 Gln Gly Gly Arg Asp Ala Arg Thr Thr Ala His Phe Lys Ala Leu Gln
 225 230 235 240
 Ala Val Ile Ala Phe Leu Leu Leu Tyr Ser Ile Phe Ile Leu Ser Leu
 245 250 255
 Leu Leu Gln Phe Trp Ile His Gly Leu Arg Lys Lys Pro Pro Phe Ile
 260 265 270
 Ala Phe Cys Gln Val Val Asp Thr Ala Phe Pro Ser Phe His Ser Tyr
 275 280 285
 Val Leu Ile Leu Arg Asp Arg Lys Leu Arg His Ala Ser Leu Ser Val
 290 295 300
 Leu Ser Trp Leu Lys Cys Arg Pro Asn Tyr Val Lys
 305 310 315

<210> 122

<211> 1339

<212> DNA

<213> Mus musculus

<400> 122

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atacatttgc aaatctttac aactaataca taaaatggag catcttttga agagaacatt 120

tgatatcacc gagaacatac ttctaattat tttattcatt gaattaataa ttggacttat 180


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aggaaacgga ttcacagcct tgggtgactg catggactgg gttaagagaa aaaaaatgtc 240
attagttaat aaaatcctca ccgctttggc aacttctaga attttcctgc tctgggtcat 300
gctagtaggt tttccaatta gctcactgta cccatattta gttactacta gactgatgat 360
acagttcact agtactctat ggactatagc taaccatatt agtgtctggg ttgctacatg 420
cctcagtgtc ttttattttc tcaagatagc caatttttct aattctcctt ttctctatct 480
aaagaggaga gttgaaaaag tagtttcagt tacattactg gtgtctctgg tcctcttggt 540
tttaaataatt ttactactta atttggaat taacatgtgt ataaatgaat atcatcaaatt 600
aaacatatca tacatcttca tttcttatta ccatttaagt tgtcaaattc aggtgttagg 660
aagtcacatt attttcctgt ctgtcccggt tgttttgtcc ctgtcaaactt ttctcctgct 720
catcttctcc ctgtggacac ttcacaagag gatgcagcag catgttcagg gaggcagaga 780
tgccagaacc acggcccact tcaaagcctt gcaagcagtg attgcctttc tcctactata 840
ctccattttt atcctgtcac tggtactaca attttggatc catggattaa ggaagaaacc 900
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ttcttagaat ttgactgcat gtatttcac ttttatttga aacaaccact aattaaagct 1140
attactaatt tagcaagtcg tatacaaggt tattttttta tacacatatc aaaaactgac 1200
atgtttatgt tctacaaaaa cctgaatata tcaaaattat ataaattttg tatcaacgat 1260
taacaatgga gtttttttat ttatgacctg tcacgggact ccggtggagt cagcttgtca 1320
gatgaaagtc tgaaagctt 1339

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<210> 123

<211> 333

<212> PRT

<213> Mus musculus

<400> 123

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Met Phe Ser Gln Ile Ile Ser Thr Ser Asp Ile Phe Thr Phe Thr Ile
1           5           10           15

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Ile Leu Phe Val Glu Leu Val Ile Gly Ile Leu Gly Asn Gly Phe Ile
          20           25           30

```

```

Ala Leu Val Asn Ile Met Asp Trp Thr Lys Arg Arg Ser Ile Ser Ser
          35           40           45

```

```

Ala Asp Gln Ile Leu Thr Ala Leu Ala Ile Thr Arg Phe Leu Tyr Val
          50           55           60

```

Trp Phe Met Ile Ile Cys Ile Leu Leu Phe Met Leu Cys Pro His Leu
 65 70 75 80
 Leu Thr Arg Ser Glu Ile Val Thr Ser Ile Gly Ile Ile Trp Ile Val
 85 90 95
 Asn Asn His Phe Ser Val Trp Leu Ala Thr Cys Leu Gly Val Phe Tyr
 100 105 110
 Phe Leu Lys Ile Ala Asn Phe Ser Asn Ser Leu Phe Leu Tyr Leu Lys
 115 120 125
 Trp Arg Val Lys Lys Val Val Leu Met Ile Ile Gln Val Ser Met Ile
 130 135 140
 Phe Leu Ile Leu Asn Leu Leu Ser Leu Ser Met Tyr Asp Gln Phe Ser
 145 150 155 160
 Ile Asp Val Tyr Glu Gly Asn Thr Ser Tyr Asn Leu Gly Asp Ser Thr
 165 170 175
 Pro Phe Pro Thr Ile Ser Leu Phe Ile Asn Ser Ser Lys Val Phe Val
 180 185 190
 Ile Thr Asn Ser Ser His Ile Phe Leu Pro Ile Asn Ser Leu Phe Met
 195 200 205
 Leu Ile Pro Phe Thr Val Ser Leu Val Ala Phe Leu Met Leu Ile Phe
 210 215 220
 Ser Leu Trp Lys His His Lys Lys Met Gln Val Asn Ala Lys Pro Pro
 225 230 235 240
 Arg Asp Ala Ser Thr Met Ala His Ile Lys Ala Leu Gln Thr Gly Phe
 245 250 255
 Ser Phe Leu Leu Leu Tyr Ala Val Tyr Leu Leu Phe Ile Val Ile Gly
 260 265 270
 Met Leu Ser Leu Arg Leu Ile Gly Gly Lys Leu Ile Leu Leu Phe Asp
 275 280 285
 His Ile Ser Gly Ile Gly Phe Pro Ile Ser His Ser Phe Val Leu Ile
 290 295 300
 Leu Gly Asn Asn Lys Leu Arg Gln Ala Ser Leu Ser Val Leu His Cys
 305 310 315 320
 Leu Arg Cys Arg Ser Lys Asp Met Asp Thr Met Gly Pro
 325 330

<210> 124

<211> 1371

<212> DNA

<213> Mus musculus

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<400> 124
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ctgggattgt ttatatattgt tacaacaaaa tttatatgtt tgtagtcag taatgtataa      180
gtgggatttt aaagcatgat tatcttgaat ttttaacaaa aaacatgtag tgctttttaa      240
atgtagcaga aacattaata attgaagcat gttctcacag ataataagca ccagtgatat      300
ttttactttt acaataatat tatttgtgga attagtaata ggaatttttag gaaatggatt      360
catagcacta gtgaatatca tggactggac caagagaaga agcatttcat cagcggatca      420
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tattatttgg atagtgaata accatttcag cgtttggctt gccacatgcc tcggtgtctt      600
ttattttctg aagatagcca atttttctaa ctctttgttt ctttacctaa agtggagagt      660
taaaaaagta gttttaatga taatacaggt atcaatgatt ttcttgattt taaacctgtt      720
atctctaagc atgtatgata agttctcaat tgatgtttat gaaggaaata catcttataa      780
tttaggggat tcaaccccat ttcccacaat ttcttattc atcaattcat caaaagtttt      840
cgtaatcacc aactcatccc atattttctt acccatcaac tccctgttca tgctcatacc      900
cttcacagtg tccctggtag cctttctcat gctcatcttc tcaactgtga agcatcacia      960
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cttgcaaaca gggttctcct tctgtctgct gtatgcagta tacttacttt ttattgtcat     1080
aggaatgttg agccttaggt tgataggagg aaaattaata cttttatttg accacatttc     1140
tggaataggt tttcctataa gccactcatt tgtgctgatt ctgggaaata acaagctgag     1200
acaagccagt ctttcagtgt tgcattgtct gaggtgccga tccaaagata tggacaccat     1260
gggtccataa aaaatttcag aggtcattgg gaaacatttt gagatcttat aggggaaaaa     1320
gaaaatgtgg ggcttcaaag ctggtaggag taatatagag aaggatagga g               1371

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<210> 125

<211> 303

<212> PRT

<213> Mus musculus

<220>

<221> MOD_RES

<222> (169)..(169)

<223> Variable amino acid

<400> 125

Met	Glu	His	Pro	Leu	Arg	Arg	Thr	Phe	Asp	Phe	Ser	Gln	Ser	Ile	Leu
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Leu	Thr	Ile	Leu	Phe	Ile	Glu	Leu	Ile	Ile	Gly	Leu	Ile	Arg	Asn	Gly
			20					25					30		
Leu	Met	Val	Leu	Val	His	Cys	Ile	Asp	Trp	Val	Lys	Arg	Lys	Lys	Phe
		35					40					45			
His	Leu	Leu	Ile	Lys	Ser	Ser	Pro	Leu	Trp	Gln	Thr	Ser	Arg	Ile	Cys
	50					55					60				
Leu	Leu	Trp	Phe	Met	Leu	Ile	His	Leu	Leu	Ile	Thr	Leu	Leu	Tyr	Ala
65					70					75					80
Asp	Leu	Ala	Ser	Thr	Arg	Thr	Met	Met	Gln	Phe	Ala	Ser	Asn	Pro	Trp
				85					90					95	
Thr	Ile	Ser	Asn	His	Ile	Ser	Ile	Trp	Leu	Ala	Thr	Cys	Leu	Gly	Val
			100					105					110		
Phe	Tyr	Phe	Leu	Lys	Ile	Ala	Asn	Phe	Ser	Asn	Ser	Thr	Phe	Leu	Tyr
		115					120					125			
Leu	Lys	Trp	Arg	Val	Gln	Phe	Leu	Leu	Leu	Asn	Ile	Leu	Leu	Val	Lys
	130					135					140				
Phe	Glu	Ile	Asn	Met	Trp	Ile	Asn	Glu	Tyr	His	Gln	Ile	Asn	Ile	Pro
145					150					155					160
Tyr	Ser	Phe	Ile	Ser	Tyr	Tyr	Gln	Xaa	Cys	Gln	Ile	Gln	Val	Leu	Ser
				165					170					175	
Leu	His	Ile	Ile	Phe	Leu	Ser	Val	Pro	Phe	Ile	Leu	Ser	Leu	Ser	Thr
			180					185					190		
Phe	Leu	Leu	Leu	Ile	Phe	Ser	Leu	Trp	Thr	Leu	His	Gln	Arg	Met	Gln
		195					200					205			
Gln	His	Val	Gln	Gly	Tyr	Arg	Asp	Ala	Ser	Thr	Met	Ala	His	Phe	Lys
	210					215					220				
Ala	Leu	Gln	Ala	Val	Ile	Ala	Phe	Leu	Leu	Ile	His	Ser	Ile	Phe	Ile
225					230					235					240
Leu	Ser	Leu	Leu	Leu	Gln	Leu	Trp	Lys	His	Glu	Leu	Arg	Lys	Lys	Pro
				245					250					255	
Pro	Phe	Val	Val	Phe	Cys	Gln	Val	Ala	Tyr	Ile	Ala	Phe	Pro	Ser	Ser
			260					265					270		
His	Ser	Tyr	Val	Phe	Ile	Leu	Gly	Asp	Arg	Lys	Leu	Arg	Gln	Ala	Cys
		275					280					285			
Leu	Ser	Val	Leu	Trp	Arg	Leu	Lys	Cys	Arg	Pro	Asn	Tyr	Val	Gly	
		290				295					300				

<210> 126
 <211> 1108
 <212> DNA
 <213> Mus musculus

<400> 126
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 tagaactaat aaataaaatg gagcatcctt tgaggagaac atttgatttc tcccagagca 180
 tacttctaac catttttattc attgaattaa taattggact tataagaaat ggattaatgg 240
 tattggtgca ctgcatagat tgggttaaga gaaaaaaatt tcatttgta atcaaatacct 300
 caccactttg gcaaacttcc agaatttgtc tgctctggtt catgctaata catctcctga 360
 ttactttatt gtatgcagat ttagctagta ctagaacgat gatgcaattc gctagcaatc 420
 catggactat atctaaccat atcagcatct ggcttgctac atgccttggt gtcttttatt 480
 ttctcaagat agccaatttt tctaactcta cttttctcta tctaaaatgg cgagttcagt 540
 tcctcttggt aaatatTTTA ctgggttaaT ttgagattaa catgtggata aatgaatatc 600
 atcaaataaa cataccatac agcttcattt cttattacca aattgtcaaa tacagggtgtt 660
 aagtcttcac attattttcc tgtctgtccc ctttattttg tccctgtcaa cttttctcct 720
 gctcatcttc tccctgtgga cacttcacca gaggatgcag cagcatgttc aaggatacag 780
 agatgccagc acaatggccc acttcaaagc cttgcaagca gtgattgcct ttctcttaat 840
 acactccatt tttatcctgt cactgttact acaactttgg aaacatgaat taaggaagaa 900
 acctcctttt gttgtatttt gtcaggttgc atatatagct tttccttcat cccattcata 960
 tgtcttcatt ctgggagaca gaaagctgag acaggcttgt ctctctgtgt tgtggaggct 1020
 gaaatgcagg ccaaattatg tgggataaaa tctctttgtg ctttcatttc caattcttaa 1080
 atattccttg attttgactg cataaatt 1108

<210> 127
 <211> 150
 <212> PRT
 <213> Mus musculus

<400> 127
 Gly Ala Ile Val Asn Val Asp Phe Leu Ile Gly Asn Val Gly Asn Gly
 1 5 10 15
 Phe Ile Val Val Ala Asn Ile Met Asp Leu Val Lys Arg Arg Lys Leu
 20 25 30

Ser Ser Val Asp Gln Leu Leu Thr Ala Leu Ala Val Ser Arg Ile Thr
 35 40 45
 Leu Leu Trp Tyr Leu Tyr Ile Met Lys Arg Thr Phe Leu Val Asp Pro
 50 55 60
 Asn Ile Gly Ala Ile Met Gln Ser Thr Arg Leu Thr Asn Val Ile Trp
 65 70 75 80
 Ile Ile Ser Asn His Phe Ser Ile Trp Leu Ala Thr Thr Leu Ser Ile
 85 90 95
 Phe Tyr Phe Leu Lys Ile Ala Asn Phe Ser Asn Ser Ile Phe Cys Tyr
 100 105 110
 Leu Arg Trp Arg Phe Glu Lys Val Ile Leu Met Ala Leu Leu Val Ser
 115 120 125
 Leu Val Leu Leu Phe Ile Asp Ile Leu Val Thr Asn Met Tyr Ile Asn
 130 135 140
 Ile Trp Thr Asp Glu Phe
 145 150

<210> 128
 <211> 520
 <212> DNA
 <213> Mus musculus

<400> 128
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 cattgttggtg gcaaacataa tggacttggg caagagaaga aagctttctt cagtggatca 180
 gctgctcact gcaactggcg tctccagaat cactttgctg tggtagctgt acataatgaa 240
 acgaacatctt ttagtggatc caaacattgg tgcaattatg caatcaacaa gactgactaa 300
 tgttatctgg ataatttcta accatttttag tatatggctg gccaccaccc tcagcatctt 360
 ttattttctc aagatagcaa atttttctaa ctctatcttc tgttacctga ggtggagatt 420
 tgaaaagggtg attttgatgg cattgctggg gtccctgggc ctcttggtta tagatatctt 480
 agtaacaaac atgtacatta atatttggac tgatgaattc 520

<210> 129
 <211> 309
 <212> PRT
 <213> Mus musculus

<400> 129
 Met Val Ala Val Leu Gln Ser Thr Leu Pro Ile Ile Phe Ser Met Glu
 1 5 10 15

Phe Ile Met Gly Thr Leu Gly Asn Gly Phe Ile Phe Leu Ile Val Cys
 20 25 30
 Ile Asp Trp Val Gln Arg Arg Lys Ile Ser Leu Val Asp Gln Ile Arg
 35 40 45
 Thr Ala Leu Ala Ile Ser Arg Ile Ala Leu Ile Trp Leu Ile Phe Leu
 50 55 60
 Asp Trp Trp Val Ser Val His Tyr Pro Ala Leu His Glu Thr Gly Lys
 65 70 75 80
 Met Leu Ser Thr Tyr Leu Ile Ser Trp Thr Val Ile Asn His Cys Asn
 85 90 95
 Phe Trp Leu Thr Ala Asn Leu Ser Ile Leu Tyr Phe Leu Lys Ile Ala
 100 105 110
 Asn Phe Ser Asn Ile Ile Phe Leu Tyr Leu Lys Phe Arg Ser Lys Asn
 115 120 125
 Val Val Leu Val Thr Leu Leu Val Ser Leu Phe Phe Leu Phe Leu Asn
 130 135 140
 Thr Val Ile Ile Lys Ile Phe Ser Asp Val Cys Phe Asp Ser Val Gln
 145 150 155 160
 Arg Asn Val Ser Gln Ile Phe Ile Met Tyr Asn His Glu Gln Ile Cys
 165 170 175
 Lys Phe Leu Ser Phe Thr Asn Pro Met Phe Thr Phe Ile Pro Phe Val
 180 185 190
 Met Ser Thr Val Met Phe Ser Leu Leu Ile Phe Ser Leu Trp Arg His
 195 200 205
 Leu Lys Asn Met Gln His Thr Ala Lys Gly Cys Arg Asp Ile Ser Thr
 210 215 220
 Thr Val His Ile Arg Ala Leu Gln Thr Ile Ile Val Ser Val Val Leu
 225 230 235 240
 Tyr Thr Ile Phe Phe Leu Ser Phe Phe Val Lys Val Trp Ser Phe Val
 245 250 255
 Ser Pro Glu Arg Tyr Leu Ile Phe Leu Phe Val Trp Ala Leu Gly Asn
 260 265 270
 Ala Val Phe Ser Ala His Pro Phe Val Met Ile Leu Val Asn Arg Arg
 275 280 285
 Leu Arg Leu Ala Ser Leu Ser Leu Ile Phe Trp Leu Trp Tyr Arg Phe
 290 295 300
 Lys Asn Ile Glu Val
 305

<210> 130
 <211> 1199
 <212> DNA
 <213> Mus musculus

<400> 130
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 agttacctca gaagtttggg tattgtttta cagaaaatgg tggcagttct acagagcaca 240
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<210> 131
 <211> 309
 <212> PRT
 <213> Mus musculus

<400> 131
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[illegible]

<210> 132

<211> 1535

<212> DNA

<213> Mus musculus

<400> 132

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caagtaaaac atacaaaaca aatactttaa tttgcctatt aacaaatggc aagaaaagat	240
tcaggcttga acatcctgta gacaagctaa ggacaggagc aactgaaggg atctccatga	300
agacctttca gattttctacc aaaagtaatt tttaactata tttaagtctt taaagaaaga	360
aagtaaagcc actcttttat tgaacagcaa tagattggaa tcttaacaa ctgcaacaga	420
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caactagtga ggctgtgctg ggcattgtag ggaacacatt cattgcactt gtaaactgta	540
tggactataa caggaacaag aagctctcta atattggctt tattctcact ggcttggcaa	600
tttccagaat ttgccttgtag ttgatcttaa tcacagaggc atacataaaa atattctatc	660
cacagttgct gtctcctgtc aacataattg agctcatcag ttatctatgg ataattatct	720
gtcaattgaa tgtctgggtt gccactagtc tcagtatttt ttatttcctg aagatagcaa	780
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taatcattaa ctatgttttc accaatgggg gagtattttt attttttatg ataatgttaa	1020
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<210> 133
 <211> 310
 <212> PRT
 <213> Mus musculus

<400> 133

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			20					25					30		
Met	Asp	Leu	Arg	Lys	Arg	Arg	Thr	Phe	Pro	Ser	Ala	Asp	His	Phe	Leu
	35						40					45			
Thr	Ala	Leu	Ala	Ile	Ser	Arg	Leu	Ala	Leu	Ile	Trp	Val	Leu	Phe	Leu
	50					55					60				
Asp	Ser	Phe	Leu	Phe	Ile	Gln	Ser	Pro	Leu	Leu	Met	Thr	Arg	Asn	Thr
65					70					75					80
Leu	Arg	Leu	Ile	Gln	Thr	Ala	Trp	Asn	Ile	Ser	Asn	His	Phe	Ser	Ile
				85					90					95	
Trp	Phe	Ala	Thr	Ser	Leu	Ser	Ile	Phe	Tyr	Leu	Phe	Lys	Ile	Ala	Ile
			100					105					110		
Phe	Ser	Asn	Tyr	Leu	Phe	Phe	Tyr	Leu	Lys	Arg	Arg	Val	Lys	Arg	Val
		115					120					125			
Val	Leu	Val	Ile	Leu	Leu	Leu	Ser	Met	Ile	Leu	Leu	Phe	Phe	Asn	Ile
	130					135					140				
Phe	Leu	Glu	Ile	Lys	His	Ile	Asp	Val	Trp	Ile	Tyr	Gly	Thr	Lys	Arg
145					150					155					160
Asn	Ile	Thr	Asn	Gly	Leu	Ser	Ser	Asn	Ser	Phe	Ser	Glu	Phe	Ser	Arg
				165					170					175	
Leu	Ile	Leu	Ile	Pro	Ser	Leu	Met	Phe	Thr	Leu	Val	Pro	Phe	Gly	Val
			180					185					190		
Ser	Leu	Ile	Ala	Phe	Leu	Leu	Leu	Ile	Phe	Ser	Leu	Met	Lys	His	Val
	195						200					205			
Arg	Lys	Met	Gln	Tyr	Tyr	Thr	Lys	Gly	Cys	Lys	Asp	Val	Arg	Thr	Met
	210					215					220				
Ala	His	Thr	Thr	Ala	Leu	Gln	Thr	Val	Val	Ala	Phe	Leu	Leu	Leu	Tyr
225					230					235					240
Thr	Thr	Phe	Phe	Leu	Ser	Leu	Val	Val	Glu	Val	Ser	Thr	Leu	Glu	Met
				245					250					255	
Asp	Glu	Ser	Leu	Met	Leu	Leu	Phe	Ala	Lys	Val	Thr	Ile	Met	Ile	Phe
			260					265					270		

Pro Ser Ile His Ser Cys Ile Phe Ile Leu Lys His Asn Lys Leu Arg
 275 280 285

Gln Asp Leu Leu Ser Val Leu Lys Trp Leu Gln Tyr Trp Cys Lys Arg
 290 295 300

Glu Lys Thr Leu Asp Ser
 305 310

<210> 134

<211> 1482

<212> DNA

<213> Mus musculus

<400> 134

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taaaaccaaa agtaaatacac aggtaaatct tctttatttt tcttttttaa tactgtatat      360
ggacattttt taatacagca tttttttttt ttgaaattta gaaaaaaacc actaagaaat      420
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actgacaatc attttcattt tggagttctt cattggaaat ctggggaatg gattcatagc      540
tctggtacaa tgcattggact tacgaaagag aagaacgttc ccttcagcag atcatttcct      600
cactgctctg gccatctcca ggcttgctct gatatggggt ttatttctag attcatttct      660
gtttatacaa tccccattac tgatgactag aaatacatta agactgattc agactgcctg      720
gaatataagc aatcatttca gtatatgggt tgctaccagc ctcagcatct tttatctctt      780
caagatagcc attttttcta actatctttt cttctacctg aagcggagag ttaaaagggt      840
ggttttggtg atactgctgc tatccatgat ctttttggtt tttaatatat ttttagaaat      900
caaacatatt gatgtctgga tctatggaac caaaagaaac ataactaatg gtttgagttc      960
aaacagtttt tcagagtttt ccaggcttat ttaattcca agtttaatgt tcacattagt     1020
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aaggaagatg cagtactaca ccaaaggatg caaagatgtc agaaccatgg cccacaccac     1140
agccctgcag actgtgggtg ccttcctcct attatatact actttctttc tgtctctagt     1200
tgtggaagtt tcaacacttg aaatggatga aagtctgatg cttctgtttg caaaagttac     1260

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<210> 135
<211> 305
<212> PRT
<213> Mus musculus

<400> 135
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Lys Asp Leu Val Lys Gly Arg Lys Ile Ser Ser Val Asp Gln Ile Leu
35 40 45
Thr Ala Leu Ala Ile Ser Arg Ile Ala Leu Leu Trp Leu Ile Leu Val
50 55 60
Ser Trp Trp Ile Phe Val Leu Tyr Pro Gly Gln Trp Met Thr Asp Arg
65 70 75 80
Arg Val Ser Ile Met His Ser Ile Trp Thr Thr Phe Asn Gln Ser Ser
85 90 95
Leu Trp Phe Ala Thr Ser Leu Ser Ile Phe Tyr Phe Phe Lys Ile Ala
100 105 110
Asn Phe Ser Asn Pro Ile Phe Leu Tyr Leu Lys Val Arg Leu Lys Lys
115 120 125
Val Met Ile Gly Thr Leu Ile Met Ser Leu Ile Leu Phe Cys Leu Asn
130 135 140
Ile Ile Ile Met Asn Ala Pro Glu Asn Ile Leu Ile Thr Glu Tyr Asn
145 150 155 160
Val Ser Met Ser Tyr Ser Leu Ile Leu Asn Asn Thr Gln Leu Ser Met
165 170 175
Leu Phe Pro Phe Ala Asn Thr Met Phe Gly Phe Ile Pro Phe Ala Val
180 185 190
Ser Leu Val Thr Phe Val Leu Leu Val Phe Ser Leu Trp Lys His Gln
195 200 205
Arg Lys Met Gln His Ser Ala His Gly Cys Arg Asp Ala Ser Thr Lys
210 215 220

Ala His Ile Arg Ala Leu Gln Thr Leu Ile Ala Ser Leu Leu Leu Tyr
 225 230 235 240

Ser Ile Phe Phe Leu Ser His Val Met Lys Val Trp Ser Ala Leu Leu
 245 250 255

Leu Glu Arg Thr Leu Leu Leu Leu Ile Thr Gln Val Ala Arg Thr Ala
 260 265 270

Phe Pro Ser Val His Ser Trp Val Leu Ile Leu Gly Asn Ala Lys Met
 275 280 285

Arg Lys Ala Ser Leu Tyr Val Phe Leu Trp Leu Arg Cys Arg His Lys
 290 295 300

Glu
 305

<210> 136

<211> 1316

<212> DNA

<213> Mus musculus

<400> 136

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gaatggtgtc ctacaggtta catttatagt cattttgagt gtggaattta taattggcat      240
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<210> 137

<211> 330

<212> PRT

<213> Mus musculus

<400> 137

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          20          25          30

Phe Met Val Leu Val His Cys Met Asp Trp Val Lys Lys Lys Lys Met
          35          40          45

Ser Leu Val Asn Gln Ile Leu Thr Ala Leu Ser Ile Ser Arg Ile Phe
          50          55          60

Gln Leu Cys Leu Leu Phe Ile Ser Leu Val Ile Asn Phe Ser Tyr Thr
65          70          75          80

Asp Leu Thr Thr Ser Ser Arg Met Ile Gln Val Met Tyr Asn Ala Trp
          85          90          95

Ile Leu Ala Asn His Phe Ser Ile Trp Ile Ala Thr Cys Leu Thr Val
          100         105         110

Leu Tyr Phe Leu Lys Ile Ala Asn Phe Ser Asn Ser Phe Phe Leu Tyr
          115         120         125

Leu Lys Trp Arg Val Glu Lys Val Val Ser Val Thr Leu Leu Val Ser
130         135         140

Leu Leu Leu Leu Ile Leu Asn Ile Leu Leu Thr Asn Leu Glu Thr Asp
145         150         155         160

Met Trp Thr Asn Glu Tyr Gln Arg Asn Ile Ser Cys Ser Phe Ser Ser
          165         170         175

His Tyr Tyr Ala Lys Cys His Arg Gln Val Leu Arg Leu His Ile Ile
          180         185         190

Phe Leu Ser Val Pro Val Val Leu Ser Leu Ser Thr Phe Leu Leu Leu
195         200         205

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Ile Phe Ser Leu Trp Thr His His Lys Arg Met Gln Gln His Val Gln
 210 215 220
 Gly Gly Arg Asp Ala Arg Thr Thr Ala His Phe Lys Ala Leu Gln Thr
 225 230 235 240
 Val Ile Ala Phe Phe Leu Leu Tyr Ser Ile Phe Ile Leu Ser Val Leu
 245 250 255
 Ile Gln Ile Trp Lys Tyr Glu Leu Leu Lys Lys Asn Leu Phe Val Val
 260 265 270
 Phe Cys Glu Val Val Tyr Ile Ala Phe Pro Thr Phe His Ser Tyr Ile
 275 280 285
 Leu Ile Val Gly Asp Met Lys Leu Arg Gln Ala Cys Leu Pro Leu Cys
 290 295 300
 Ile Ile Ala Ala Glu Ile Gln Thr Thr Leu Cys Arg Asn Phe Arg Ser
 305 310 315 320
 Leu Lys Tyr Phe Arg Leu Cys Cys Ile Phe
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<210> 138

<211> 1354

<212> DNA

<213> Mus musculus

<400> 138

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agaaaaatac attttatgag aatcaactca gaggttgtca gaaattgtcg aaacagcatt	180
ttaaaaaattt acatctcaac tggatatatg agcaagtctt tataactgat atataaaatg	240
aagcactttt ggaagatatt atctgttatc tcccagagca cactttcagt cattttaatc	300
gtggaattag taattggaat tataggaaat gggttcatgg tcttgggtcca ctgtatggac	360
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ccgacattcc attcatatat tctgattgta ggagacatga agctgagaca ggctgcctg      1140
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aagtacttta gattatgttg tatattctag acaaaaatta actgatacaa atgtcttttg      1260
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<210> 139

<211> 299

<212> PRT

<213> Mus musculus

<400> 139

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Phe Arg Glu Trp Met His Phe Gln Arg Leu Ser Pro Val Glu Thr Ile
35        40        45

Leu Ile Ser Leu Gly Ile Ser His Phe Cys Leu Gln Trp Thr Ser Met
50        55        60

Leu Tyr Asn Phe Gly Thr Tyr Ser Arg Pro Val Leu Leu Phe Trp Lys
65        70        75        80

Val Ser Val Val Trp Glu Phe Met Asn Ile Leu Thr Phe Trp Leu Thr
85        90        95

Ser Trp Leu Ala Val Leu Tyr Cys Val Lys Val Ser Ser Phe Thr His
100       105       110

Pro Ile Phe Leu Trp Leu Arg Met Lys Ile Leu Lys Leu Val Leu Trp
115       120       125

Leu Ile Leu Gly Ala Leu Ile Ala Ser Cys Leu Ser Ile Ile Pro Ser
130       135       140

Val Val Lys Tyr His Ile Gln Met Glu Leu Val Thr Leu Asp Asn Leu
145       150       155       160

Pro Lys Asn Asn Ser Leu Ile Leu Arg Leu Gln Gln Phe Glu Trp Tyr
165       170       175

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Phe Ser Asn Pro Leu Lys Met Ile Gly Phe Gly Ile Pro Phe Phe Val
 180 185 190
 Phe Leu Ala Ser Ile Ile Leu Leu Thr Val Ser Leu Val Gln His Trp
 195 200 205
 Val Gln Met Lys His Tyr Ser Ser Ser Asn Ser Ser Leu Lys Ala Gln
 210 215 220
 Phe Thr Val Leu Lys Ser Leu Ala Thr Phe Phe Thr Phe Phe Thr Ser
 225 230 235 240
 Tyr Phe Leu Thr Ile Val Ile Ser Phe Ile Gly Thr Val Phe Asp Lys
 245 250 255
 Lys Ser Trp Phe Trp Val Cys Glu Ala Val Ile Tyr Gly Leu Val Cys
 260 265 270
 Ile His Phe Thr Ser Leu Met Met Ser Asn Pro Ala Leu Lys Lys Ala
 275 280 285
 Leu Lys Leu Gln Phe Trp Ser Pro Glu Pro Ser
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<210> 140
 <211> 2887
 <212> DNA
 <213> Mus musculus

<220>
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 aatcaattcc ttaattataa gctattgttt cattatttca tttcctacgt ttttttgcac 180
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<210> 141

<211> 335

<212> PRT

<213> Mus musculus

<400> 141

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 Ile Asp Leu Ile Met Trp Lys Lys Met Ala Pro Leu Asp Leu Leu Leu
 35 40 45
 Phe Cys Leu Ala Thr Ser Arg Ile Ile Leu Gln Leu Cys Ile Leu Phe
 50 55 60
 Ala Gln Leu Gly Leu Ser Cys Leu Val Arg His Thr Leu Phe Ala Asp
 65 70 75 80
 Asn Val Thr Phe Val Tyr Ile Ile Asn Glu Leu Ser Leu Trp Phe Ala
 85 90 95
 Thr Trp Leu Gly Val Phe Tyr Cys Ala Lys Ile Ala Thr Ile Pro His
 100 105 110
 Pro Leu Phe Leu Trp Leu Lys Met Arg Ile Ser Arg Leu Val Pro Trp
 115 120 125
 Leu Ile Leu Ala Ser Val Val Tyr Val Thr Val Thr Thr Phe Ile His
 130 135 140
 Ser Arg Glu Thr Ser Glu Leu Pro Lys Gln Ile Phe Ile Ser Phe Phe
 145 150 155 160
 Ser Lys Asn Thr Thr Arg Val Arg Pro Ala His Ala Thr Leu Leu Ser
 165 170 175

Val Phe Val Phe Gly Leu Thr Leu Pro Phe Leu Ile Phe Thr Val Ala
180 185 190

Val Leu Leu Leu Leu Ser Ser Leu Trp Asn His Ser Arg Gln Met Arg
195 , 200 205

Thr Met Val Gly Thr Arg Glu Pro Ser Arg His Ala Leu Val Ser Ala
210 215 220

Met Leu Ser Ile Leu Ser Phe Leu Ile Leu Tyr Leu Ser His Asp Met
225 230 235 240

Val Ala Val Leu Ile Cys Thr Gln Gly Leu His Phe Gly Ser Arg Thr
245 250 255

Phe Ala Phe Cys Leu Leu Val Ile Gly Met Tyr Pro Ser Leu His Ser
260 265 270

Ile Val Leu Ile Leu Gly Asn Pro Lys Leu Lys Arg Asn Ala Lys Thr
275 280 285

Phe Ile Val His Cys Lys Cys Cys His Cys Ala Arg Ala Trp Val Thr
290 295 300

Ser Arg Asn Pro Arg Leu Ser Asp Leu Pro Val Pro Ala Thr His His
305 310 315 320

Ser Ala Asn Lys Thr Ser Cys Ser Glu Ala Cys Ile Met Pro Ser
325 330 335

<210> 142

<211> 1698

<212> DNA

<213> Mus musculus

<400> 142

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tctatggtat ctcttcctta tttgactgac attgagttga gaaggcagca ctataaacia      360
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atttaaagaa gtcattgggtt cttcttattt taaaatgatg gaaggtcata tgctcttctt      540
ccttctggtc gtggtagtgc agtttttaac tggggtcttg gcaaatggcc tcattgtggt      600

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cagtatgatt tgctgcag 1698

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<210> 143

<211> 295

<212> PRT

<213> Mus musculus

<400> 143

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Met Asn Leu Val Glu Trp Ile Val Thr Ile Ile Met Met Thr Glu Phe
1           5           10           15

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Leu Leu Gly Asn Cys Ala Asn Val Phe Ile Thr Ile Val Asn Phe Ile
20           25           30

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Asp Cys Val Lys Arg Arg Lys Ile Ser Ser Ala Asp Arg Ile Ile Thr
35           40           45

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Ala Ile Ala Ile Phe Arg Ile Gly Leu Leu Trp Ala Met Leu Thr Asn
50           55           60

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Trp His Ser His Val Phe Thr Pro Asp Thr Asp Asn Leu Gln Met Arg
 65 70 75 80
 Val Phe Gly Gly Ile Thr Trp Ala Ile Thr Asn His Phe Thr Thr Trp
 85 90 95
 Leu Gly Thr Ile Leu Ser Met Phe Tyr Leu Phe Lys Ile Ala Asn Phe
 100 105 110
 Ser Asn Ser Leu Phe Leu His Leu Lys Arg Lys Leu Asp Asn Val Leu
 115 120 125
 Leu Val Ile Phe Leu Gly Ser Ser Leu Phe Leu Val Ala Tyr Leu Gly
 130 135 140
 Met Val Asn Ile Lys Lys Ile Ala Trp Met Ser Ile His Glu Gly Asn
 145 150 155 160
 Val Thr Thr Lys Ser Lys Leu Lys His Val Thr Ser Ile Thr Asn Met
 165 170 175
 Leu Leu Phe Ser Leu Ile Asn Ile Val Pro Phe Gly Ile Ser Leu Asn
 180 185 190
 Cys Val Leu Leu Leu Ile Tyr Ser Leu Ser Lys His Leu Lys Asn Met
 195 200 205
 Lys Phe Tyr Gly Lys Gly Cys Gln Asp Gln Ser Thr Met Val His Ile
 210 215 220
 Lys Ala Leu Gln Thr Val Val Ser Phe Leu Leu Leu Tyr Ala Thr Tyr
 225 230 235 240
 Ser Ser Cys Val Ile Ile Ser Gly Trp Ser Leu Gln Asn Ala Pro Val
 245 250 255
 Phe Leu Phe Cys Val Thr Ile Gly Ser Phe Tyr Pro Ala Gly His Ser
 260 265 270
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<210> 144

<211> 1394

<212> DNA

<213> Mus musculus

<400> 144

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atttgaagca atggaccaga attcctcttt atttgactct tagcaaattg gaatgcagca 180

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<210> 145

<211> 305

<212> PRT

<213> Mus musculus

<400> 145

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Met Gly Ser Asn Val Tyr Gly Ile Leu Thr Met Val Met Ile Ala Glu
1           5           10           15

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Phe Val Phe Gly Asn Met Ser Asn Gly Phe Ile Val Leu Ile Asn Cys
20           25           30

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Ile Asp Trp Val Arg Lys Gly Thr Leu Ser Ser Ile Gly Trp Ile Leu
35           40           45

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Leu Phe Leu Ala Ile Ser Arg Met Val Leu Ile Trp Glu Met Leu Ile
 50 55 60
 Thr Trp Ile Lys Tyr Met Lys Tyr Ser Phe Ser Phe Val Thr Gly Thr
 65 70 75 80
 Glu Leu Arg Gly Ile Met Phe Thr Trp Val Ile Ser Asn His Phe Ser
 85 90 95
 Leu Trp Leu Ala Thr Ile Leu Ser Ile Phe Tyr Leu Leu Lys Ile Ala
 100 105 110
 Ser Phe Ser Lys Pro Val Phe Leu Tyr Leu Lys Trp Arg Glu Lys Lys
 115 120 125
 Val Leu Leu Ile Val Leu Leu Gly Asn Leu Ile Phe Leu Met Leu Asn
 130 135 140
 Ile Leu Gln Ile Asn Lys His Ile Glu His Trp Met Tyr Gln Tyr Glu
 145 150 155 160
 Arg Asn Ile Thr Trp Ser Ser Arg Val Ser Asp Phe Ala Gly Phe Ser
 165 170 175
 Asn Leu Val Leu Leu Glu Met Ile Val Phe Ser Val Thr Pro Phe Thr
 180 185 190
 Val Ala Leu Val Ser Phe Ile Leu Leu Ile Phe Ser Leu Trp Lys His
 195 200 205
 Leu Gln Lys Met His Leu Asn Ser Arg Gly Glu Arg Asp Pro Ser Thr
 210 215 220
 Lys Ala His Val Asn Ala Leu Arg Ile Met Val Ser Phe Leu Leu Leu
 225 230 235 240
 Tyr Ala Thr Tyr Phe Ile Ser Phe Phe Leu Ser Leu Ile Pro Met Ala
 245 250 255
 His Lys Thr Arg Leu Gly Leu Met Phe Ser Ile Thr Val Gly Leu Phe
 260 265 270
 Tyr Pro Ser Ser His Ser Phe Ile Leu Ile Leu Gly His Ser Asn Leu
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 His
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<210> 146

<211> 2567

<212> DNA

<213> Mus musculus

<400> 146
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 aaagcattag aatttcacta ttccataagg cagccaaacc acgtgctact aggtatatga 1740

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<210> 147

<211> 309

<212> PRT

<213> Mus musculus

<400> 147

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Phe Ile Ile Gly Thr Leu Gly Asn Gly Phe Ile Val Leu Ile Asn Ser
20          25          30

Thr Ser Trp Phe Lys Asn Gln Lys Ile Ser Val Ile Asp Phe Ile Leu
35          40          45

Thr Trp Leu Ala Ile Ser Arg Met Cys Val Leu Trp Thr Thr Ile Ala
50          55          60

Gly Ala Ser Leu Arg Lys Phe Tyr Lys Thr Leu Ser Tyr Ser Lys Asn
65          70          75          80

Phe Lys Phe Cys Phe Asp Ile Ile Trp Thr Gly Ser Asn Tyr Leu Cys
85          90          95

Ile Ala Cys Thr Thr Cys Ile Ser Val Phe Tyr Leu Phe Lys Ile Ala
100         105         110

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Asn Phe Ser Asn Ser Ile Phe Phe Trp Ile Lys Gln Arg Ile His Ala
 115 120 125
 Val Leu Leu Ala Ile Val Leu Gly Thr Leu Met Tyr Phe Ile Leu Phe
 130 135 140
 Leu Ile Phe Met Lys Met Ile Ala Asn Asn Phe Ile Tyr Lys Trp Thr
 145 150 155 160
 Lys Leu Glu Gln Asn Thr Thr Phe Pro Val Leu Asp Thr Leu Ser Gly
 165 170 175
 Phe Leu Val Tyr His Ser Leu Tyr Asn Gly Ile Leu Ile Phe Phe Phe
 180 185 190
 Ile Val Ser Leu Thr Ser Phe Leu Leu Leu Ile Phe Ser Leu Trp Ser
 195 200 205
 His Leu Arg Arg Met Lys Leu Gln Gly Ile His Thr Lys Asp Ile Ser
 210 215 220
 Thr Glu Ala His Ile Lys Ala Met Lys Thr Met Met Ser Phe Leu Leu
 225 230 235 240
 Phe Phe Ile Ile Tyr Tyr Ile Ser Asn Ile Met Leu Ile Val Ala Ser
 245 250 255
 Ser Ile Leu Asp Asn Val Val Ala Gln Ile Phe Ser Tyr Asn Leu Ile
 260 265 270
 Phe Leu Tyr Leu Ser Val His Pro Phe Leu Leu Val Leu Trp Asn Ser
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 Lys Leu Lys Trp Thr Phe Gln His Val Leu Arg Lys Leu Val Cys His
 290 295 300
 Cys Gly Gly Tyr Ser
 305

<210> 148

<211> 1488

<212> DNA

<213> Mus musculus

<400> 148

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tcattgccca ttttaagattt ggattcacac atctacatca atgtggctgt aatccatttt	300
cccatgatga aataaggtag agactgccta ttaaacgaca tgtcgagcct actggagatt	360

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<210> 149

<211> 333

<212> PRT

<213> Mus musculus

<400> 149

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Met Phe Ser Gln Lys Ile Asn Tyr Ser His Leu Phe Thr Phe Ser Ile
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Thr Leu Tyr Val Glu Ile Val Thr Gly Ile Leu Gly His Gly Phe Ile
20           25           30

Ala Leu Val Asn Ile Met Asp Trp Val Lys Arg Arg Arg Ile Ser Ser
35           40           45

Val Asp Gln Ile Leu Thr Ala Leu Ala Leu Thr Arg Phe Ile Tyr Val
50           55           60

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Leu	Ser	Met	Leu	Ile	Cys	Ile	Leu	Leu	Phe	Met	Leu	Cys	Pro	His	Leu
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Pro	Arg	Arg	Ser	Glu	Met	Leu	Ser	Ala	Met	Gly	Ile	Phe	Trp	Val	Val
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Asn	Ser	His	Phe	Ser	Ile	Trp	Leu	Thr	Thr	Cys	Leu	Gly	Val	Phe	Tyr
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Phe	Leu	Lys	Ile	Ala	Asn	Phe	Ser	Asn	Ser	Phe	Phe	Leu	Tyr	Leu	Lys
		115					120					125			
Trp	Arg	Val	Lys	Lys	Val	Ile	Leu	Ile	Ile	Ile	Leu	Ala	Ser	Leu	Ile
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Ile	Ala	Ala	Tyr	Val	Gly	Asn	Met	Ser	Tyr	Ser	Leu	Thr	Asp	Leu	Thr
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Gln	Phe	Ser	Ser	Thr	Phe	Leu	Phe	Ser	Asn	Ser	Ser	Asn	Val	Phe	Leu
			180					185					190		
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		195					200					205			
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	210					215					220				
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225					230					235					240
Arg	Asp	Val	Ser	Thr	Met	Ala	His	Ile	Lys	Ala	Leu	Gln	Thr	Val	Phe
				245					250					255	
Ser	Phe	Leu	Leu	Leu	Tyr	Ala	Ile	Tyr	Leu	Leu	Phe	Leu	Ile	Ile	Gly
		260					265						270		
Ile	Leu	Asn	Leu	Gly	Leu	Met	Glu	Lys	Ile	Val	Ile	Leu	Ile	Phe	Asp
	275						280					285			
His	Ile	Ser	Gly	Ala	Val	Phe	Pro	Ile	Ser	His	Ser	Phe	Val	Leu	Ile
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Leu	Gly	Asn	Ser	Lys	Leu	Arg	Gln	Ala	Ser	Leu	Ser	Val	Leu	Pro	Cys
305					310					315					320
Leu	Arg	Cys	Gln	Ser	Lys	Asp	Met	Asp	Thr	Met	Gly	Leu			
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<211> 1442

<212> DNA

<213> Mus musculus

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<210> 151
 <211> 309
 <212> PRT
 <213> Mus musculus

<400> 151

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20          25          30

Ile Asp Trp Ile Asn Lys Lys Glu Leu Ser Thr Val Asp Gln Ile Leu
35          40          45

Ile Val Leu Ala Ile Ser Arg Ile Ser Leu Ile Trp Glu Thr Leu Ile
50          55          60

Ile Trp Val Lys Asp Gln Leu Ile Ser Ser Ile Thr Ile Glu Glu Leu
65          70          75          80

Lys Ile Ile Val Phe Ser Phe Ile Leu Ser Ser His Phe Ser Leu Trp
85          90          95

Leu Ala Thr Ala Leu Ser Ile Phe Tyr Leu Phe Arg Ile Pro Asn Cys
100         105         110

Tyr Trp Gln Ile Phe Leu Tyr Leu Lys Trp Arg Ile Lys Gln Leu Ile
115         120         125

Val His Met Leu Leu Gly Ser Leu Val Phe Leu Val Ala Asn Met Ile
130         135         140

Gln Ile Thr Ile Thr Leu Glu Glu Arg Phe Tyr Gln Tyr Gly Gly Asn
145         150         155         160

Thr Ser Val Asn Ser Met Glu Thr Glu Phe Ser Ile Leu Ile Glu Leu
165         170         175

Met Leu Phe Asn Met Thr Met Phe Ser Ile Ile Pro Phe Ser Leu Ala
180         185         190

Leu Ile Ser Phe Leu Leu Leu Ile Phe Ser Leu Trp Lys His Leu Gln
195         200         205

Lys Met Pro Leu Asn Ser Arg Gly Asp Arg Asp Pro Ser Ala Thr Ala
210         215         220

His Arg Asn Ala Leu Arg Ile Leu Val Ser Phe Leu Leu Leu Tyr Thr
225         230         235         240

Ile Tyr Phe Leu Ser Leu Leu Ile Ser Trp Val Ala Gln Lys Asn Gln
245         250         255

Ser Glu Leu Val His Ile Ile Cys Met Ile Thr Ser Leu Val Tyr Pro
260         265         270

Ser Phe His Ser Tyr Ile Leu Ile Leu Gly Asn Tyr Lys Leu Lys Gln
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Asn Thr Pro Thr Thr
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<210> 152

<211> 1465

<212> DNA

<213> Mus musculus

<400> 152

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<210> 153

<211> 311

<212> PRT

<213> Mus musculus

<400> 153

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Ile Ile Asp Trp Val Lys Arg Arg Lys Ile Ser Leu Met Asp Lys Ile
35 40 45

Ile Thr Ala Leu Ala Ile Ser Arg Ile Tyr Leu Leu Trp Ser Thr Phe
50 55 60

Leu Ile Thr Leu Thr Ser Ser Leu Asp Pro Asp Ile Lys Met Ala Val
65 70 75 80

Lys Ile Ile Arg Ile Ser Asn Asn Thr Trp Ile Ile Ala Asn His Phe
85 90 95

Ser Ile Trp Phe Ala Thr Cys Leu Ser Ile Phe Tyr Phe Leu Lys Ile
100 105 110

Ala Asn Phe Ser Asn Tyr Ile Phe Leu Tyr Leu Arg Trp Arg Phe Lys
115 120 125

Lys Val Val Ser Val Thr Leu Leu Ile Ser Leu Ile Phe Leu Leu Leu
130 135 140

Asn Ile Leu Leu Met Asn Met His Ile Asp Ile Trp Ser Asp Lys Ser
145 150 155 160

Lys Arg Asn Leu Ser Phe Ser Val Arg Ser Asn Asn Cys Thr Gln Phe
165 170 175

Pro Arg Leu Val Leu Leu Ile Asn Thr Met Phe Thr Ser Ile Pro Phe
180 185 190

Thr Val Ser Leu Leu Ala Phe Leu Leu Leu Ile Phe Ser Leu Trp Arg
195 200 205

His Leu Lys Thr Met Gln Tyr Tyr Ala Lys Gly Ser Glu Asp Thr Thr
210 215 220

Thr Ala Ala His Ile Lys Ala Leu His Met Val Val Ala Phe Leu Leu
225 230 235 240

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<210> 154
<211> 1103
<212> DNA
<213> Mus musculus
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<210> 155
<211> 308
<212> PRT
<213> Mus musculus

<400> 155
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Arg Glu Trp Leu Leu Arg Gly Arg Leu Leu Pro Ser Asp Met Ile Leu
35 40 45
Phe Ser Leu Gly Thr Ser Arg Phe Phe Gln Gln Cys Val Gly Leu Val
50 55 60
Asn Ser Phe Tyr Tyr Phe Leu His Leu Val Glu Tyr Ser Gly Ser Leu
65 70 75 80
Ala Arg Gln Leu Ile Ser Leu His Trp Asp Phe Leu Asn Ser Ala Thr
85 90 95
Phe Trp Phe Cys Thr Trp Leu Ser Val Leu Phe Cys Ile Lys Ile Ala
100 105 110
Asn Phe Ser His Pro Ala Phe Leu Trp Leu Lys Trp Arg Phe Pro Ala
115 120 125
Leu Val Pro Trp Phe Leu Leu Gly Ser Ile Leu Val Ser Val Ile Val
130 135 140
Thr Leu Leu Phe Phe Trp Gly Asn His Thr Ile Tyr Gln Ala Phe Leu
145 150 155 160
Arg Arg Lys Phe Thr Gly Asn Thr Thr Phe Lys Glu Trp Asn Arg Arg
165 170 175
Leu Glu Ile Asp Tyr Phe Met Pro Leu Lys Val Val Thr Met Ser Ile
180 185 190
Pro Cys Ser Leu Phe Leu Val Ser Ile Leu Leu Leu Ile Ser Ser Leu
195 200 205
Arg Arg His Ser Leu Arg Met Gln His Asn Thr His Ser Leu Gln Asp
210 215 220
Pro Asn Val Gln Ala His Ser Arg Ala Leu Lys Ser Leu Ile Ser Phe
225 230 235 240
Leu Val Leu Tyr Ala Val Ser Phe Val Ser Met Ile Ile Asp Ala Thr
245 250 255

Val Phe Ile Ser Ser Asp Asn Val Trp Tyr Trp Pro Trp Gln Ile Ile
 260 265 270

Leu Tyr Phe Cys Met Ser Val His Pro Phe Ile Leu Ile Thr Asn Asn
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Phe Trp Val Ala
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<210> 156
 <211> 3437
 <212> DNA
 <213> Mus musculus

<400> 156
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<210> 157
 <211> 340
 <212> DNA
 <213> Mus musculus

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tatgccactg gtaaagaaat gagaatcatt gacttcttct ggacactaac caatcactta 240
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<210> 158
 <211> 82
 <212> PRT
 <213> Mus musculus

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Val His Asn Phe Tyr Tyr Ser Ala Gln Lys Val Glu Tyr Ser Gly Gly
           35           40           45
Leu Gly Arg Gln Phe Phe His Leu His Trp His Phe Leu Asn Ser Ala
50           55           60

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Ala Asn

<210> 159
 <211> 341
 <212> DNA
 <213> Mus musculus

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<210> 160
 <211> 320
 <212> PRT
 <213> Mus musculus

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 Ile His Trp Tyr Lys Arg Arg Lys Ile Ser Ala Leu Asn Gln Ile Leu
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 Thr Ala Leu Ala Phe Ser Arg Ile Tyr Leu Leu Leu Thr Val Phe Thr
 50 55 60
 Val Ile Ala Val Ser Thr Leu Tyr Thr His Val Leu Val Thr Arg Arg
 65 70 75 80
 Val Val Lys Leu Ile Asn Phe His Leu Leu Phe Ser Asn His Phe Ser
 85 90 95
 Met Trp Leu Ala Ala Cys Leu Gly Leu Tyr Tyr Phe Leu Lys Ile Ala
 100 105 110
 His Phe Pro Asn Ser Ile Phe Val Tyr Leu Lys Met Arg Ile Asn Gln
 115 120 125
 Val Val Ser Gly Thr Leu Leu Met Ser Leu Gly Leu Leu Phe Leu Asn
 130 135 140

Thr Leu Leu Ile Asn Ser Tyr Ile Asp Thr Lys Ile Asp Asp Tyr Arg
 145 150 155 160
 Glu His Leu Leu Tyr Asp Phe Thr Ser Asn Asn Thr Ala Ser Phe Tyr
 165 170 175
 Arg Val Ile Leu Val Ile Asn Asn Cys Ile Phe Thr Ser Ile Pro Phe
 180 185 190
 Thr Leu Ser Gln Ser Thr Phe Leu Leu Leu Ile Phe Ser Leu Trp Arg
 195 200 205
 His Tyr Lys Lys Met Gln Gln His Ala Gln Arg Cys Arg Asp Val Leu
 210 215 220
 Ala Asp Ala His Ile Arg Val Leu Gln Thr Met Val Thr Tyr Val Leu
 225 230 235 240
 Leu Cys Ala Ile Phe Phe Leu Ser Leu Ser Met Gln Ile Leu Arg Ser
 245 250 255
 Glu Leu Leu Lys Asn Ile Leu Tyr Val Arg Phe Cys Glu Ile Val Ala
 260 265 270
 Ala Val Phe Pro Ser Gly His Ser Cys Val Leu Ile Cys Arg Asp Thr
 275 280 285
 Asn Leu Arg Gly Thr Phe Leu Ser Val Leu Ser Trp Leu Lys Gln Arg
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 Phe Thr Ser Trp Ile Pro Asn Ile Asn Cys Arg Ser Ser Cys Ile Phe
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<210> 161

<211> 1108

<212> DNA

<213> Mus musculus

<400> 161

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acaagagaag aaagatctct gcactgaatc aaatactcac agccttggtt ttctccagaa      300
tctaccttct tttaacagta ttactgtta tagcagtgtc tacgctatac acacacgtgt      360
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gcatgtggct tgctgcatgc cttggccttt attattttct taaaatagct ctttttcccta      480
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<210> 162

<211> 312

<212> PRT

<213> Mus musculus

<400> 162

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20          25          30
Met Gly Trp Met Lys Asn Arg Lys Ile Ala Ser Ile Asp Leu Ile Leu
35          40          45
Ser Ser Val Ala Met Ser Arg Ile Cys Leu Gln Cys Ile Ile Leu Leu
50          55          60
Asp Cys Ile Ile Leu Val Gln Tyr Pro Asp Thr Tyr Asn Arg Gly Lys
65          70          75          80
Glu Met Arg Thr Val Asp Phe Phe Trp Thr Leu Thr Asn His Leu Ser
85          90          95
Val Trp Phe Ala Thr Cys Leu Ser Ile Phe Tyr Leu Phe Lys Ile Ala
100         105         110
Asn Phe Phe His Pro Leu Phe Leu Trp Ile Lys Trp Arg Ile Asp Lys
115         120         125
Leu Ile Leu Arg Thr Leu Leu Ala Cys Val Ile Ile Ser Leu Cys Phe
130         135         140
Ser Leu Pro Val Thr Glu Asn Leu Ser Asp Asp Phe Arg Arg Cys Val
145         150         155         160

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Lys Thr Lys Glu Arg Ile Asn Ser Thr Leu Arg Cys Lys Val Asn Lys
 165 170 175
 Ala Gly His Ala Ser Val Lys Val Asn Leu Asn Leu Val Met Leu Phe
 180 185 190
 Pro Phe Ser Val Ser Leu Val Ser Phe Leu Leu Leu Ile Leu Ser Leu
 195 200 205
 Trp Arg His Thr Arg Gln Ile Gln Leu Ser Val Thr Gly Tyr Lys Asp
 210 215 220
 Pro Ser Thr Thr Ala His Val Lys Ala Met Lys Ala Val Ile Ser Phe
 225 230 235 240
 Leu Ala Leu Phe Val Val Tyr Cys Leu Ala Phe Leu Ile Ala Thr Ser
 245 250 255
 Ser Tyr Phe Met Pro Glu Ser Glu Leu Ala Val Ile Trp Gly Glu Leu
 260 265 270
 Ile Ala Leu Ile Tyr Pro Ser Ser His Ser Phe Ile Leu Ile Leu Gly
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<210> 163

<211> 3775

<212> DNA

<213> Mus musculus

<400> 163

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<210> 164

<211> 310

<212> PRT

<213> Mus musculus

<400> 164

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<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic T2R
Family Consensus Sequence 1

<220>

<221> MOD_RES

<222> (2)

<223> Phe or Ala

<220>

<221> MOD_RES

<222> (3)

<223> Ile, Val or Leu

<220>

<221> MOD_RES

<222> (4)

<223> Val or Leu

<220>

<221> MOD_RES

<222> (6)

<223> Ile or Val

<220>

<221> MOD_RES

<222> (7)

<223> Leu or Val

<220>

<221> MOD_RES

<222> (10)

<223> Gly or Thr

<220>

<221> MOD_RES

<222> (13)

<223> Val or Ala

<220>

<221> MOD_RES

<222> (18)

<223> Ile or Met

<400> 166

Glu Xaa Xaa Xaa Gly Xaa Xaa Gly Asn Xaa Phe Ile Xaa Leu Val Asn
1 5 10 15

Cys Xaa Asp Trp
20

<210> 167
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic T2R
Family Consensus Sequence 2

<220>
<221> MOD_RES
<222> (1)
<223> Asp or Gly

<220>
<221> MOD_RES
<222> (2)
<223> Phe or Leu

<220>
<221> MOD_RES
<222> (3)
<223> Ile or Leu

<220>
<221> MOD_RES
<222> (5)
<223> Thr or Ile

<220>
<221> MOD_RES
<222> (6)
<223> Gly, Ala or Ser

<220>
<221> MOD_RES
<222> (13)
<223> Cys, Gly or Phe

<400> 167
Xaa Xaa Xaa Leu Xaa Xaa Leu Ala Ile Ser Arg Ile Xaa Leu
1 5 10

<210> 168
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic T2R
Family Consensus Sequence 3

<220>
 <221> MOD_RES
 <222> (3)
 <223> Leu or Phe

<220>
 <221> MOD_RES
 <222> (4)
 <223> Ser, Thr or Asn

<220>
 <221> MOD_RES
 <222> (5)
 <223> Leu, Ile or Val

<220>
 <221> MOD_RES
 <222> (7)
 <223> Phe or Leu

<220>
 <221> MOD_RES
 <222> (8)
 <223> Ala or Thr

<220>
 <221> MOD_RES
 <222> (10)
 <223> Cys, Ser or Asn

<220>
 <221> MOD_RES
 <222> (12)
 <223> Ser, Asn or Gly

<220>
 <221> MOD_RES
 <222> (13)
 <223> Ile or Val

<400> 168
 Asn His Xaa Xaa Xaa Trp Xaa Xaa Thr Xaa Leu Xaa Xaa
 1 5 10

<210> 169
 <211> 18
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic T2R
 Family Consensus Sequence 4

<220>
 <221> MOD_RES
 <222> (2)
 <223> Phe or Cys

<220>
 <221> MOD_RES
 <222> (7)
 <223> Asn or Ser

<220>
 <221> MOD_RES
 <222> (10)
 <223> His or Asn

<220>
 <221> MOD_RES
 <222> (11)
 <223> Pro or Ser

<220>
 <221> MOD_RES
 <222> (12)
 <223> Leu, Ile or Val

<220>
 <221> MOD_RES
 <222> (15)
 <223> Trp or Tyr

<400> 169
 Phe Tyr Xaa Leu Lys Ile Ala Xaa Phe Ser Xaa Xaa Xaa Phe Leu Xaa
 1 5 10 15

Leu Lys

<210> 170
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic T2R
 Family Consensus Sequence 5

<220>
 <221> MOD_RES
 <222> (4)
 <223> Ile, Phe or Val

<220>
 <221> MOD_RES
 <222> (8)
 <223> Lys or Arg

<220>
 <221> MOD_RES
 <222> (10)
 <223> Ser or Thr

<220>
 <221> MOD_RES
 <222> (11)
 <223> Lys or Arg

<220>
 <221> MOD_RES
 <222> (12)
 <223> Gln or Lys

<220>
 <221> MOD_RES
 <222> (13)
 <223> Met or Ile

<220>
 <221> MOD_RES
 <222> (14)
 <223> Gln or Lys

<400> 170
 Leu Leu Ile Xaa Ser Leu Trp Xaa His Xaa Xaa Xaa Xaa Xaa
 1 5 10

<210> 171
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic T2R
 Family Consensus Sequence 6

<220>
 <221> MOD_RES
 <222> (3)
 <223> Phe or Leu

<220>
 <221> MOD_RES
 <222> (4)
 <223> Ile or Val

<220>
 <221> MOD_RES
 <222> (7)
 <223> Leu or Met

<220>
 <221> MOD_RES
 <222> (8)
 <223> Gly, Ser or Thr

<220>
 <221> MOD_RES
 <222> (10)
 <223> Pro, Ser or Asn

<220>
 <221> MOD_RES
 <222> (13)
 <223> Lys or Arg

<220>
 <221> MOD_RES
 <222> (14)
 <223> Gln or Arg

<400> 171
 His Ser Xaa Xaa Leu Ile Xaa Xaa Asn Xaa Lys Leu Xaa Xaa
 1 5 10

<210> 172
 <211> 1002
 <212> DNA
 <213> Homo sapiens

<400> 172
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 atttcagtcc tggagtttgc agtgggggtt ctgaccaatg ccttcgtttt cttggtgaat 120
 ttttgggatg tagtgaagag gcaggcactg agcaacagtg attgtgtgct gctgtgtctc 180
 agcatcagcc ggcttttctt gcatggactg ctgttcttga gtgctatcca gcttaccac 240
 ttccagaagt tgagtgaacc actgaaccac agctaccaag ccatcatcat gctatggatg 300
 attgcaaacc aagccaacct ctggcttgct gcctgcctca gcctgcttta ctgctccaag 360
 ctcatccgtt tctctcacac cttcctgata tgcttggcaa gctgggtctc caggaagatc 420
 tcccagatgc tcctgggtat tattctttgc tcctgcatct gcaactgtct ctgtgtttgg 480
 tgctttttta gcagacctca cttcacagtc acaactgtgc tattcatgaa taacaatata 540
 aggctcaact ggcagattaa agatctcaat ttattttatt cctttctctt ctgctatctg 600
 tggctctgtgc ctcttttctt attgtttctg gtttcttctg ggatgctgac tgtctccctg 660
 ggaaggcaca tgaggacaat gaaggcttat accagaaact ctctgaccc cagcctggag 720
 gccacatta aagccctcaa gtctcttgct tcctttttct gcttctttgt gatatcatcc 780
 tgtgttgctt tcatctctgt gccctactg attctgtggc gcgacaaaat aggggtgatg 840
 gtttgtgttg ggataatggc agcttgtccc tctgggcatg cagccatcct gatctcaggc 900
 aatgccaagt tgaggagagc tgtgatgacc attctgctct gggctcagag cagcctgaag 960
 gtaagagccg accacaaggc agattcccgg acactgtgct ga 1002

<210> 173
 <211> 333
 <212> PRT
 <213> Homo sapiens

<400> 173

Met	Leu	Thr	Leu	Thr	Arg	Ile	Arg	Thr	Val	Ser	Tyr	Glu	Val	Arg	Ser
1				5					10					15	
Thr	Phe	Leu	Phe	Ile	Ser	Val	Leu	Glu	Phe	Ala	Val	Gly	Phe	Leu	Thr
			20					25					30		
Asn	Ala	Phe	Val	Phe	Leu	Val	Asn	Phe	Trp	Asp	Val	Val	Lys	Arg	Gln
		35					40					45			
Ala	Leu	Ser	Asn	Ser	Asp	Cys	Val	Leu	Leu	Cys	Leu	Ser	Ile	Ser	Arg
	50					55					60				
Leu	Phe	Leu	His	Gly	Leu	Leu	Phe	Leu	Ser	Ala	Ile	Gln	Leu	Thr	His
65					70					75				80	
Phe	Gln	Lys	Leu	Ser	Glu	Pro	Leu	Asn	His	Ser	Tyr	Gln	Ala	Ile	Ile
				85					90					95	
Met	Leu	Trp	Met	Ile	Ala	Asn	Gln	Ala	Asn	Leu	Trp	Leu	Ala	Ala	Cys
			100					105					110		
Leu	Ser	Leu	Leu	Tyr	Cys	Ser	Lys	Leu	Ile	Arg	Phe	Ser	His	Thr	Phe
		115					120					125			
Leu	Ile	Cys	Leu	Ala	Ser	Trp	Val	Ser	Arg	Lys	Ile	Ser	Gln	Met	Leu
	130					135					140				
Leu	Gly	Ile	Ile	Leu	Cys	Ser	Cys	Ile	Cys	Thr	Val	Leu	Cys	Val	Trp
145					150					155				160	
Cys	Phe	Phe	Ser	Arg	Pro	His	Phe	Thr	Val	Thr	Thr	Val	Leu	Phe	Met
				165					170					175	
Asn	Asn	Asn	Thr	Arg	Leu	Asn	Trp	Gln	Ile	Lys	Asp	Leu	Asn	Leu	Phe
			180					185					190		
Tyr	Ser	Phe	Leu	Phe	Cys	Tyr	Leu	Trp	Ser	Val	Pro	Pro	Phe	Leu	Leu
		195					200					205			
Phe	Leu	Val	Ser	Ser	Gly	Met	Leu	Thr	Val	Ser	Leu	Gly	Arg	His	Met
	210					215					220				
Arg	Thr	Met	Lys	Val	Tyr	Thr	Arg	Asn	Ser	Arg	Asp	Pro	Ser	Leu	Glu
225					230					235				240	
Ala	His	Ile	Lys	Ala	Leu	Lys	Ser	Leu	Val	Ser	Phe	Phe	Cys	Phe	Phe
				245					250					255	
Val	Ile	Ser	Ser	Cys	Val	Ala	Phe	Ile	Ser	Val	Pro	Leu	Leu	Ile	Leu
			260					265					270		

Trp Arg Asp Lys Ile Gly Val Met Val Cys Val Gly Ile Met Ala Ala
 275 280 285

Cys Pro Ser Gly His Ala Ala Ile Leu Ile Ser Gly Asn Ala Lys Leu
 290 295 300

Arg Arg Ala Val Met Thr Ile Leu Leu Trp Ala Gln Ser Ser Leu Lys
 305 310 315 320

Val Arg Ala Asp His Lys Ala Asp Ser Arg Thr Leu Cys
 325 330

<210> 174
 <211> 966
 <212> DNA
 <213> Homo sapiens

<400> 174
 atgactaaac tctgcatcc tgcagaaagt gaattgtcgc cattttctcat caccttaatt 60
 ttagcagttt tacttgctga atacctcatt ggtatcattg caaatgggtt catcatggct 120
 atacatgcag ctgaatgggt tcaaaataag gcagtttcca caagtggcag gatcctgggt 180
 ttcctgagtg tatccagaat agctctccaa agcctcatga tgtagaaat taccatcagc 240
 tcaacctccc taagttttta ttctgaagac gctgtatatt atgcattcaa aataagtttt 300
 atattcttaa atttttgtag cctgtgggtt gctgcctggc tcagtttctt ctactttgtg 360
 aagattgcca atttctccta ccccttttct ctcaaactga ggtggagaat tactggattg 420
 ataccctggc ttctgtggct gtccgtgttt atttccttca gtcacagcat gttctgcac 480
 aacatctgca ctgtgtattg taacaattct ttccctatcc actcctccaa ctccactaag 540
 aaaacatact tgtctgagat caatgtgggt ggtctggctt ttttctttaa cctggggatt 600
 gtgactcctc tgatcatgtt catcctgaca gccaccctgc tgatcctctc tctcaagaga 660
 cacaccctac acatgggaag caatgccaca ggtccaacg accccagcat ggaggctcac 720
 atggggggcca tcaaagctat cagctacttt ctatttctt acattttcaa tgcagttgct 780
 ctgtttatct acctgtccaa catgtttgac atcaacagtc tgtggaataa tttgtgccag 840
 atcatcatgg ctgcctaccc tgccagccac tcaattctac tgattcaaga taaccctggg 900
 ctgagaagag cctggaagcg gcttcagctt cgacttcac tttacccaaa agagtggact 960
 ctgtga 966

<210> 175
 <211> 321
 <212> PRT
 <213> Homo sapiens

<400> 175

Met	Thr	Lys	Leu	Cys	Asp	Pro	Ala	Glu	Ser	Glu	Leu	Ser	Pro	Phe	Leu
1				5					10					15	
Ile	Thr	Leu	Ile	Leu	Ala	Val	Leu	Leu	Ala	Glu	Tyr	Leu	Ile	Gly	Ile
		20						25					30		
Ile	Ala	Asn	Gly	Phe	Ile	Met	Ala	Ile	His	Ala	Ala	Glu	Trp	Val	Gln
		35					40					45			
Asn	Lys	Ala	Val	Ser	Thr	Ser	Gly	Arg	Ile	Leu	Val	Phe	Leu	Ser	Val
	50					55					60				
Ser	Arg	Ile	Ala	Leu	Gln	Ser	Leu	Met	Met	Leu	Glu	Ile	Thr	Ile	Ser
65					70					75					80
Ser	Thr	Ser	Leu	Ser	Phe	Tyr	Ser	Glu	Asp	Ala	Val	Tyr	Tyr	Ala	Phe
			85						90					95	
Lys	Ile	Ser	Phe	Ile	Phe	Leu	Asn	Phe	Cys	Ser	Leu	Trp	Phe	Ala	Ala
			100					105					110		
Trp	Leu	Ser	Phe	Phe	Tyr	Phe	Val	Lys	Ile	Ala	Asn	Phe	Ser	Tyr	Pro
		115					120					125			
Leu	Phe	Leu	Lys	Leu	Arg	Trp	Arg	Ile	Thr	Gly	Leu	Ile	Pro	Trp	Leu
	130					135					140				
Leu	Trp	Leu	Ser	Val	Phe	Ile	Ser	Phe	Ser	His	Ser	Met	Phe	Cys	Ile
145					150					155					160
Asn	Ile	Cys	Thr	Val	Tyr	Cys	Asn	Asn	Ser	Phe	Pro	Ile	His	Ser	Ser
			165						170					175	
Asn	Ser	Thr	Lys	Lys	Thr	Tyr	Leu	Ser	Glu	Ile	Asn	Val	Val	Gly	Leu
		180						185					190		
Ala	Phe	Phe	Phe	Asn	Leu	Gly	Ile	Val	Thr	Pro	Leu	Ile	Met	Phe	Ile
		195					200					205			
Leu	Thr	Ala	Thr	Leu	Leu	Ile	Leu	Ser	Leu	Lys	Arg	His	Thr	Leu	His
	210					215					220				
Met	Gly	Ser	Asn	Ala	Thr	Gly	Ser	Asn	Asp	Pro	Ser	Met	Glu	Ala	His
225					230					235					240
Met	Gly	Ala	Ile	Lys	Ala	Ile	Ser	Tyr	Phe	Leu	Ile	Leu	Tyr	Ile	Phe
			245						250					255	
Asn	Ala	Val	Ala	Leu	Phe	Ile	Tyr	Leu	Ser	Asn	Met	Phe	Asp	Ile	Asn
		260						265					270		
Ser	Leu	Trp	Asn	Asn	Leu	Cys	Gln	Ile	Ile	Met	Ala	Ala	Tyr	Pro	Ala
		275					280					285			
Ser	His	Ser	Ile	Leu	Leu	Ile	Gln	Asp	Asn	Pro	Gly	Leu	Arg	Arg	Ala
	290					295					300				

Trp Lys Arg Leu Gln Leu Arg Leu His Leu Tyr Pro Lys Glu Trp Thr
 305 310 315 320

Leu

<210> 176

<211> 972

<212> DNA

<213> Homo sapiens

<400> 176

atggcaacgg tgaacacaga tgccacagat aaagacatat ccaagttcaa ggtcaccttc	60
actttgggtgg tctccggaat agagtgcac actggcatcc ttgggagtgg cttcatcacg	120
gccatctatg gggctgagtg ggccaggggc aaaacactcc ccaactgggtga ccgcattatg	180
ttgatgctga gcttttccag gctcttgcta cagatttggga tgatgctgga gaacattttc	240
agtctgctat tccgaattgt ttataaccaa aactcagtgt atatcctctt caaagtcac	300
actgtctttc tgaaccattc caatctctgg tttgctgcct ggctcaaagt cttctattgt	360
cttagaattg caaacttcaa tcatcctttg ttcttctga tgaagaggaa aatcatagt	420
ctgatgcctt ggcttctcag gctgtcagt ttggtttctt taagcttcag ctttctctc	480
tcgagagatg tcttcaatgt gtatgtgaat agctccattc ctatccctc ctccaactcc	540
acggagaaga agtacttctc tgagaccaat atgggtcaacc tggatatttt ctataacatg	600
gggatcttcg ttctctgat catgttcac ctggcagcca ccctgctgat cctctctctc	660
aagagacaca ccctacacat gggaagcaat gccacagggt ccaggggacc cagcatgaag	720
gctcacatag gggccatcaa agccaccagc tacttttctc tctctacat tttcaatgca	780
attgctctat ttctttccac gtccaacatc tttgacactt acagttcctg gaatattttg	840
tgcaagatca tcatggctgc ctaccctgcc ggccactcag tacaactgat cttgggcaac	900
cctgggctga gaagagcctg gaagcgggtt cagcaccaag ttctctttta cctaaaagg	960
cagactctgt ga	972

<210> 177

<211> 323

<212> PRT

<213> Homo sapiens

<400> 177

Met Ala Thr Val Asn Thr Asp Ala Thr Asp Lys Asp Ile Ser Lys Phe
1 5 10 15

Gln Thr Leu

<210> 178
 <211> 930
 <212> DNA
 <213> Homo sapiens

<400> 178
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 aatttttgcta atggccttcat agcactggta aattccattg agtgggtcaa gagacaaaag 120
 atctcctttg ctgaccaa atctcactgct ctggcggtct ccagagttgg ttgctctggt 180
 gtattattat taaactggta ttcaactgtg ttgaatccag cttttaatag tgtagaagta 240
 agaactactg cttataatat ctgggcagtg atcaaccatt tcagcaactg gcttgctact 300
 accctcagca tattttatatt gctcaagatt gccaatctct ccaactttat ttttcttcac 360
 ttaaagagga gagttaagag tgtcattctg gtgatgttgt tggggccttt gctatttttg 420
 gcttgctatc tttttgtgat aaacatgaat gagattgtgc ggacaaaaga atttgaagga 480
 aacatgactt ggaagatcaa attgaagagt gcaatgtact tttcaaatat gactgtaacc 540
 atggtagcaa acttagtacc cttcactctg accctactat cttttatgct gttaatctgt 600
 tctttgtgta aacatctcaa gaagatgcag ctccatggta aaggatctca agatcccagc 660
 accaaggtcc acataaaagc tttgcaaact gtgatctcct tctcttgggt atgtgccatt 720
 tactttctgt ccataatgat atcagtttgg agttttggaa gtctggaaaa caaacctgtc 780
 ttcatgttct gcaaagctat tagattcagc tatccttcaa tccaccatt catcctgatt 840
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 gtgaaaggag agaagacttc atctccatag 930

<210> 179
 <211> 309
 <212> PRT
 <213> Homo sapiens

<400> 179
 Met Ile Thr Phe Leu Pro Ile Ile Phe Ser Ser Leu Val Val Val Thr
 1 5 10 15
 Phe Val Ile Gly Asn Phe Ala Asn Gly Phe Ile Ala Leu Val Asn Ser
 20 25 30
 Ile Glu Trp Phe Lys Arg Gln Lys Ile Ser Phe Ala Asp Gln Ile Leu
 35 40 45
 Thr Ala Leu Ala Val Ser Arg Val Gly Leu Leu Trp Val Leu Leu Leu
 50 55 60

Asn Trp Tyr Ser Thr Val Leu Asn Pro Ala Phe Asn Ser Val Glu Val
 65 70 75 80
 Arg Thr Thr Ala Tyr Asn Ile Trp Ala Val Ile Asn His Phe Ser Asn
 85 90 95
 Trp Leu Ala Thr Thr Leu Ser Ile Phe Tyr Leu Leu Lys Ile Ala Asn
 100 105 110
 Phe Ser Asn Phe Ile Phe Leu His Leu Lys Arg Arg Val Lys Ser Val
 115 120 125
 Ile Leu Val Met Leu Leu Gly Pro Leu Leu Phe Leu Ala Cys His Leu
 130 135 140
 Phe Val Ile Asn Met Asn Glu Ile Val Arg Thr Lys Glu Phe Glu Gly
 145 150 155 160
 Asn Met Thr Trp Lys Ile Lys Leu Lys Ser Ala Met Tyr Phe Ser Asn
 165 170 175
 Met Thr Val Thr Met Val Ala Asn Leu Val Pro Phe Thr Leu Thr Leu
 180 185 190
 Leu Ser Phe Met Leu Leu Ile Cys Ser Leu Cys Lys His Leu Lys Lys
 195 200 205
 Met Gln Leu His Gly Lys Gly Ser Gln Asp Pro Ser Thr Lys Val His
 210 215 220
 Ile Lys Ala Leu Gln Thr Val Ile Ser Phe Leu Leu Leu Cys Ala Ile
 225 230 235 240
 Tyr Phe Leu Ser Ile Met Ile Ser Val Trp Ser Phe Gly Ser Leu Glu
 245 250 255
 Asn Lys Pro Val Phe Met Phe Cys Lys Ala Ile Arg Phe Ser Tyr Pro
 260 265 270
 Ser Ile His Pro Phe Ile Leu Ile Trp Gly Asn Lys Lys Leu Lys Gln
 275 280 285
 Thr Phe Leu Ser Val Phe Trp Gln Met Arg Tyr Trp Val Lys Gly Glu
 290 295 300
 Lys Thr Ser Ser Pro
 305

<210> 180

<211> 930

<212> DNA

<213> Homo sapiens

<400> 180

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aattttgcc aatggctttat agcactgata aatttcattg cctgggtcaa gagacaaaag 120

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atctcctcag ctgatcaaat tattgctgct ctggcagtct ccagagttgg tttgctctgg 180
gtaatattat tacattggta ttcaactgtg ttgaatccaa cttcatctaa tttaaaagta 240
ataattttta tttctaatagc ctgggcagta accaatcatt tcagcatctg gcttgctact 300
agcctcagca tattttatatt gctcaagatc gtcaatttct ccagacttat ttttcatcac 360
ttaaaaagga aggctaagag tgtagttctg gtgatagtgt tggggctctt gttctttttg 420
gtttgtcacc ttgtgatgaa acacacgtat ataaatgtgt ggacagaaga atgtgaagga 480
aacgtaactt ggaagatcaa actgaggaat gcaatgcacc tttccaactt gactgtagcc 540
atgctagcaa acttgatacc attcactctg accctgatat cttttctgct gttaatctac 600
tctctgtgta aacatctgaa gaagatgcag ctccatggca aaggatctca agatcccagc 660
accaagatcc acataaaaagc tctgcaaact gtgacctcct tcctcatatt acttgccatt 720
tactttctgt gtctaatacat atcgttttgg aattttaaga tgcgacccaaa agaaattgtc 780
ttaatgcttt gccaaagcttt tggaatcata tatccatcat tccactcatt cattctgatt 840
tgggggaaca agacgctaaa gcagaccttt ctttcagttt tgtggcaggt gacttgctgg 900
gcaaaaggac agaaccagtc aactccatag 930

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<210> 181
<211> 309
<212> PRT
<213> Homo sapiens

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<400> 181
Met Met Ser Phe Leu His Ile Val Phe Ser Ile Leu Val Val Val Ala
1          5          10          15

Phe Ile Leu Gly Asn Phe Ala Asn Gly Phe Ile Ala Leu Ile Asn Phe
20          25          30

Ile Ala Trp Val Lys Arg Gln Lys Ile Ser Ser Ala Asp Gln Ile Ile
35          40          45

Ala Ala Leu Ala Val Ser Arg Val Gly Leu Leu Trp Val Ile Leu Leu
50          55          60

His Trp Tyr Ser Thr Val Leu Asn Pro Thr Ser Ser Asn Leu Lys Val
65          70          75          80

Ile Ile Phe Ile Ser Asn Ala Trp Ala Val Thr Asn His Phe Ser Ile
85          90          95

Trp Leu Ala Thr Ser Leu Ser Ile Phe Tyr Leu Leu Lys Ile Val Asn
100         105         110

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180

Phe Ser Arg Leu Ile Phe His His Leu Lys Arg Lys Ala Lys Ser Val
 115 120 125

Val Leu Val Ile Val Leu Gly Ser Leu Phe Phe Leu Val Cys His Leu
 130 135 140

Val Met Lys His Thr Tyr Ile Asn Val Trp Thr Glu Glu Cys Glu Gly
 145 150 155 160

Asn Val Thr Trp Lys Ile Lys Leu Arg Asn Ala Met His Leu Ser Asn
 165 170 175

Leu Thr Val Ala Met Leu Ala Asn Leu Ile Pro Phe Thr Leu Thr Leu
 180 185 190

Ile Ser Phe Leu Leu Leu Ile Tyr Ser Leu Cys Lys His Leu Lys Lys
 195 200 205

Met Gln Leu His Gly Lys Gly Ser Gln Asp Pro Ser Thr Lys Ile His
 210 215 220

Ile Lys Ala Leu Gln Thr Val Thr Ser Phe Leu Ile Leu Leu Ala Ile
 225 230 235 240

Tyr Phe Leu Cys Leu Ile Ile Ser Phe Trp Asn Phe Lys Met Arg Pro
 245 250 255

Lys Glu Ile Val Leu Met Leu Cys Gln Ala Phe Gly Ile Ile Tyr Pro
 260 265 270

Ser Phe His Ser Phe Ile Leu Ile Trp Gly Asn Lys Thr Leu Lys Gln
 275 280 285

Thr Phe Leu Ser Val Leu Trp Gln Val Thr Cys Trp Ala Lys Gly Gln
 290 295 300

Asn Gln Ser Thr Pro
 305

<210> 182

<211> 930

<212> DNA

<213> Homo sapiens

<400> 182

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atctcttttg ctgaccagat tctcactgct ctggcggtct ccagagttgg tttgctctgg	180
gtattattat taaattggta ttcaactgtg tttaatccag ctttttatag tgtagaagta	240
agaactactg cttataatgt ctgggcagta accggccatt tcagcaactg gcttgctact	300
agcctcagca tattttattt gctcaagatt gccaatctct ccaaccttat ttttcttcac	360


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ttaaagagga gagttaagag tgtcattctg gtgatgctgt tggggccttt actatctttg 420
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aacttgactt ggaagatcaa attgaggagt gcagtgtacc tttcagatgc gactgtaacc 540
acgctaggaa acttagtgcc cttcactctg accctgctat gttttttgct gttaatctgt 600
tctctgtgta aacatctcaa gaagatgcag ctccatggta aaggatctca agatcccagc 660
accaaggtcc acataaaagc tttgcaaact gtgatctttt tcctcttggt atgtgccgtt 720
tactttctgt ccataatgat atcagtttgg agttttggga gtctggaaaa caaacctgtc 780
ttcatgttct gcaaagctat tagattcagc tacccttcaa tccaccatt catcctgatt 840
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gtgaaaggag agaagccttc atctccatag 930

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<210> 183
<211> 309
<212> PRT
<213> Homo sapiens

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<400> 183
Met Thr Thr Phe Ile Pro Ile Ile Phe Ser Ser Val Val Val Val Leu
1          5          10          15

Phe Val Ile Gly Asn Phe Ala Asn Gly Phe Ile Ala Leu Val Asn Ser
20          25          30

Ile Glu Arg Val Lys Arg Gln Lys Ile Ser Phe Ala Asp Gln Ile Leu
35          40          45

Thr Ala Leu Ala Val Ser Arg Val Gly Leu Leu Trp Val Leu Leu Leu
50          55          60

Asn Trp Tyr Ser Thr Val Phe Asn Pro Ala Phe Tyr Ser Val Glu Val
65          70          75          80

Arg Thr Thr Ala Tyr Asn Val Trp Ala Val Thr Gly His Phe Ser Asn
85          90          95

Trp Leu Ala Thr Ser Leu Ser Ile Phe Tyr Leu Leu Lys Ile Ala Asn
100         105         110

Phe Ser Asn Leu Ile Phe Leu His Leu Lys Arg Arg Val Lys Ser Val
115         120         125

Ile Leu Val Met Leu Leu Gly Pro Leu Leu Phe Leu Ala Cys Gln Leu
130         135         140

Phe Val Ile Asn Met Lys Glu Ile Val Arg Thr Lys Glu Tyr Glu Gly
145         150         155         160

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[illegible]

<210> 184

<211> 900

<212> DNA

<213> Homo sapiens

<400> 184

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atctcctcag	ctgagcaaat	tctcactgct	ctggtggtct	ccagaattgg	tttactctgg	180
gtcatgttat	tcctttggta	tgcaactgtg	tttaattctg	ctttatatgg	tttagaagta	240
agaattgttg	cttctaattgc	ctgggctgta	acgaaccatt	tcagcatgtg	gcttgctgct	300
agcctcagca	tattttgttt	gctcaagatt	gccaatctct	ccaaccttat	ttctctccac	360
ctaaagaaga	gaattaagag	tgttgttctg	gtgatactgt	tggggccctt	ggatattctg	420
atttgtaatc	ttgctgtgat	aaccatggat	gagagagtgt	ggacaaaaga	atatgaagga	480
aatgtgactt	ggaagatcaa	attgaggaat	gcaatacacc	tttcaagctt	gactgtaact	540
actctagcaa	acctcatacc	ctttactctg	agcctaatat	gttttctgct	gttaatctgt	600
tctctttgta	aacatctcaa	gaagatgcgg	ctccatagca	aaggatctca	agatcccagc	660

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accaaggtcc atataaaagc tttgcaaact gtgacctcct tcctcatggt atttgccatt      720
tactttctgt gtataatcac atcaacttgg aatcttagga cacagcagag caaacttgta      780
ctcctgcttt gccaaactgt tgcaatcatg tatccttcat tccactcatt catcctgatt      840
atgggaagta ggaagctaaa acagaccttt ctttcagttt tgtggcagat gacacgctga      900

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<210> 185
<211> 299
<212> PRT
<213> Homo sapiens

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<400> 185
Met Met Cys Phe Leu Leu Ile Ile Ser Ser Ile Leu Val Val Phe Ala
1          5          10          15

Phe Val Leu Gly Asn Val Ala Asn Gly Phe Ile Ala Leu Val Asn Val
20        25        30

Ile Asp Trp Val Asn Thr Arg Lys Ile Ser Ser Ala Glu Gln Ile Leu
35        40        45

Thr Ala Leu Val Val Ser Arg Ile Gly Leu Leu Trp Val Met Leu Phe
50        55        60

Leu Trp Tyr Ala Thr Val Phe Asn Ser Ala Leu Tyr Gly Leu Glu Val
65        70        75        80

Arg Ile Val Ala Ser Asn Ala Trp Ala Val Thr Asn His Phe Ser Met
85        90        95

Trp Leu Ala Ala Ser Leu Ser Ile Phe Cys Leu Leu Lys Ile Ala Asn
100       105       110

Phe Ser Asn Leu Ile Ser Leu His Leu Lys Lys Arg Ile Lys Ser Val
115       120       125

Val Leu Val Ile Leu Leu Gly Pro Leu Val Phe Leu Ile Cys Asn Leu
130       135       140

Ala Val Ile Thr Met Asp Glu Arg Val Trp Thr Lys Glu Tyr Glu Gly
145       150       155       160

Asn Val Thr Trp Lys Ile Lys Leu Arg Asn Ala Ile His Leu Ser Ser
165       170       175

Leu Thr Val Thr Thr Leu Ala Asn Leu Ile Pro Phe Thr Leu Ser Leu
180       185       190

Ile Cys Phe Leu Leu Leu Ile Cys Ser Leu Cys Lys His Leu Lys Lys
195       200       205

Met Arg Leu His Ser Lys Gly Ser Gln Asp Pro Ser Thr Lys Val His
210       215       220

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Ile Lys Ala Leu Gln Thr Val Thr Ser Phe Leu Met Leu Phe Ala Ile
 225 230 235 240
 Tyr Phe Leu Cys Ile Ile Thr Ser Thr Trp Asn Leu Arg Thr Gln Gln
 245 250 255
 Ser Lys Leu Val Leu Leu Leu Cys Gln Thr Val Ala Ile Met Tyr Pro
 260 265 270
 Ser Phe His Ser Phe Ile Leu Ile Met Gly Ser Arg Lys Leu Lys Gln
 275 280 285
 Thr Phe Leu Ser Val Leu Trp Gln Met Thr Arg
 290 295

<210> 186
 <211> 900
 <212> DNA
 <213> Homo sapiens

<400> 186
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 aactttgccca atggcttcat agcactggta aatttcattg actgggtgaa gagaaaaaag 120
 atctcctcag ctgaccaaatt tctcactgct ctggcggtct ccagaattgg tttgctctgg 180
 gcattattat taaattggta ttttaactgtg ttgaatccag ctttttatag tgtagaatta 240
 agaattactt cttataatgc ctgggttgta accaaccatt tcagcatgtg gcttgctgct 300
 aacctcagca tattttattt gctcaagatt gccaatctct ccaaccttct ttttcttcat 360
 ttaaagagga gagttaggag tgtcattctg gtgatactgt tggggacttt gatatttttg 420
 gtttgtcatc ttcttgtggc aaacatggat gagagtatgt gggcagaaga atatgaagga 480
 aacatgactg ggaagatgaa attgaggaat acagtacatc tttcatattt gactgtaact 540
 accctatgga gcttcatacc ctttactctg tccttgatat cttttctgat gctaattctgt 600
 tctctgtgta aacatctcaa gaagatgcag ctccatggag aaggatcgca agatctcagc 660
 accaaggtcc acataaaagc tttgcaaact ctgatctcct tcctcttggt atgtgccatt 720
 ttctttctat tcctaactgt ttcgggttggt agtcctagga ggctgaggaa tgacccggtt 780
 gtcattggtta gcaaggctgt tggaacata tatcttgcac tcgactcatt catcctaatt 840
 tggagaacca agaagctaaa acacaccttt cttttgattt tgtgtcagat taggtgctga 900

<210> 187
 <211> 299
 <212> PRT
 <213> Homo sapiens

<400> 187

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Met Ile Thr Phe Leu Tyr Ile Phe Phe Ser Ile Leu Ile Met Val Leu
1           5           10           15

Phe Val Leu Gly Asn Phe Ala Asn Gly Phe Ile Ala Leu Val Asn Phe
20           25           30

Ile Asp Trp Val Lys Arg Lys Lys Ile Ser Ser Ala Asp Gln Ile Leu
35           40           45

Thr Ala Leu Ala Val Ser Arg Ile Gly Leu Leu Trp Ala Leu Leu Leu
50           55           60

Asn Trp Tyr Leu Thr Val Leu Asn Pro Ala Phe Tyr Ser Val Glu Leu
65           70           75           80

Arg Ile Thr Ser Tyr Asn Ala Trp Val Val Thr Asn His Phe Ser Met
85           90           95

Trp Leu Ala Ala Asn Leu Ser Ile Phe Tyr Leu Leu Lys Ile Ala Asn
100          105          110

Phe Ser Asn Leu Leu Phe Leu His Leu Lys Arg Arg Val Arg Ser Val
115          120          125

Ile Leu Val Ile Leu Leu Gly Thr Leu Ile Phe Leu Val Cys His Leu
130          135          140

Leu Val Ala Asn Met Asp Glu Ser Met Trp Ala Glu Glu Tyr Glu Gly
145          150          155          160

Asn Met Thr Gly Lys Met Lys Leu Arg Asn Thr Val His Leu Ser Tyr
165          170          175

Leu Thr Val Thr Thr Leu Trp Ser Phe Ile Pro Phe Thr Leu Ser Leu
180          185          190

Ile Ser Phe Leu Met Leu Ile Cys Ser Leu Cys Lys His Leu Lys Lys
195          200          205

Met Gln Leu His Gly Glu Gly Ser Gln Asp Leu Ser Thr Lys Val His
210          215          220

Ile Lys Ala Leu Gln Thr Leu Ile Ser Phe Leu Leu Leu Cys Ala Ile
225          230          235          240

Phe Phe Leu Phe Leu Ile Val Ser Val Trp Ser Pro Arg Arg Leu Arg
245          250          255

Asn Asp Pro Val Val Met Val Ser Lys Ala Val Gly Asn Ile Tyr Leu
260          265          270

Ala Phe Asp Ser Phe Ile Leu Ile Trp Arg Thr Lys Lys Leu Lys His
275          280          285

Thr Phe Leu Leu Ile Leu Cys Gln Ile Arg Cys
290          295

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<210> 188
 <211> 924
 <212> DNA
 <213> Homo sapiens

<400> 188
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 attgcagcga atggcttcat tgtgctgggtg ctgggcaggg agtggctgag atatggcagg 120
 ttgctgcctt tggatatgat cctcattagc ttgggtgcct cccgcttctg cctgcagttg 180
 gttgggacgg tgcacaactt ctactactct gcccagaagg tcgagtactc tgggggtctc 240
 ggccgacagt tcttccatct acactggcac ttctgaact cagccacctt ctggttttgc 300
 agctggctca gtgtcctggt ctgtgtgaag attgctaaca tcacacactc caccttctctg 360
 tggctgaagt ggaggttccc aggggtgggtg ccctggctcc tgttgggctc tgtcctgac 420
 tccttcatca taacctgtct gtttttttgg gtgaactacc ctgtatatca agaattttta 480
 attagaaaat tttctgggaa catgacctac aagtgggaata caaggataga aacatactat 540
 ttcccatccc tgaaactggg catctgggtca attccttttt ctgtttttct ggtctcaatt 600
 atgctgttaa ttaattctct gaggaggcat actcagagaa tgcagcacia cgggcacagc 660
 ctgcaggacc ccagcaccca ggctcacacc agagctctga agtccctcat ctcttctctc 720
 attctttatg ctctgtcctt tctgtccctg atcattgatg ccgcaaaatt tatctccatg 780
 cagaacgact tttactggcc atggcaaat gtagtctacc tgtgcatatc tgtccatccc 840
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 gcaaggggct tctgggtggc ctag 924

<210> 189
 <211> 307
 <212> PRT
 <213> Homo sapiens

<400> 189
 Met Gln Ala Ala Leu Thr Ala Phe Phe Val Leu Leu Phe Ser Leu Leu
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 Ser Leu Leu Gly Ile Ala Ala Asn Gly Phe Ile Val Leu Val Leu Gly
 20 25 30
 Arg Glu Trp Leu Arg Tyr Gly Arg Leu Leu Pro Leu Asp Met Ile Leu
 35 40 45
 Ile Ser Leu Gly Ala Ser Arg Phe Cys Leu Gln Leu Val Gly Thr Val
 50 55 60

His Asn Phe Tyr Tyr Ser Ala Gln Lys Val Glu Tyr Ser Gly Gly Leu
 65 70 75 80
 Gly Arg Gln Phe Phe His Leu His Trp His Phe Leu Asn Ser Ala Thr
 85 90 95
 Phe Trp Phe Cys Ser Trp Leu Ser Val Leu Phe Cys Val Lys Ile Ala
 100 105 110
 Asn Ile Thr His Ser Thr Phe Leu Trp Leu Lys Trp Arg Phe Pro Gly
 115 120 125
 Trp Val Pro Trp Leu Leu Leu Gly Ser Val Leu Ile Ser Phe Ile Ile
 130 135 140
 Thr Leu Leu Phe Phe Trp Val Asn Tyr Pro Val Tyr Gln Glu Phe Leu
 145 150 155 160
 Ile Arg Lys Phe Ser Gly Asn Met Thr Tyr Lys Trp Asn Thr Arg Ile
 165 170 175
 Glu Thr Tyr Tyr Phe Pro Ser Leu Lys Leu Val Ile Trp Ser Ile Pro
 180 185 190
 Phe Ser Val Phe Leu Val Ser Ile Met Leu Leu Ile Asn Ser Leu Arg
 195 200 205
 Arg His Thr Gln Arg Met Gln His Asn Gly His Ser Leu Gln Asp Pro
 210 215 220
 Ser Thr Gln Ala His Thr Arg Ala Leu Lys Ser Leu Ile Ser Phe Leu
 225 230 235 240
 Ile Leu Tyr Ala Leu Ser Phe Leu Ser Leu Ile Ile Asp Ala Ala Lys
 245 250 255
 Phe Ile Ser Met Gln Asn Asp Phe Tyr Trp Pro Trp Gln Ile Ala Val
 260 265 270
 Tyr Leu Cys Ile Ser Val His Pro Phe Ile Leu Ile Phe Ser Asn Leu
 275 280 285
 Lys Leu Arg Ser Val Phe Ser Gln Leu Leu Leu Leu Ala Arg Gly Phe
 290 295 300
 Trp Val Ala
 305

<210> 190

<211> 930

<212> DNA

<213> Homo sapiens

<400> 190

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atctcttttg ctgaccaa at tctcactgct ctggcagtct ccagagttgg tttactctgg 180
gtattagtat taaattggta tgcaactgag ttgaatccag cttttaacag tatagaagta 240
agaattactg cttacaatgt ctgggcagta atcaaccatt tcagcaactg gcttgctact 300
agcctcagca tattttat ttt gctcaagatt gccaat tttct ccaaccttat ttttcttcac 360
ttaaagagga gagttaagag tgttggtctg gtgatactat tggggccttt gctat ttttg 420
gtttgtcatc tttttgtgat aaacatgaat cagattatat ggacaaaaga atatgaagga 480
aacatgactt ggaagatcaa actgaggagt gcaatgtacc tttcaaatac aacggtaacc 540
atcctagcaa acttagttcc cttcactctg accctgatat cttttctgct gttaatctgt 600
tctctgtgta aacatctcaa aaagatgcag ctccatggca aaggatctca agatcccagc 660
atgaagg tcc acataaaagc tttgcaaact gtgacctcct tcctcttggt atgtgccatt 720
tactttctgt ccataatcat gtcagtttgg agttttgaga gtctggaaaa caaacctgtc 780
ttcatgttct gccaa gctat tgcattcagc tatccttcaa cccacccatt catcctgatt 840
tggggaaaca agaagctaaa gcagactttt ctttcagttt tgtggcatgt gaggtactgg 900
gtgaaaggag agaagccttc atcttcatag 930

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<210> 191

<211> 309

<212> PRT

<213> Homo sapiens

<400> 191

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Met Ile Thr Phe Leu Pro Ile Ile Phe Ser Ile Leu Ile Val Val Thr
1          5          10          15

Phe Val Ile Gly Asn Phe Ala Asn Gly Phe Ile Ala Leu Val Asn Ser
20          25          30

Ile Glu Trp Phe Lys Arg Gln Lys Ile Ser Phe Ala Asp Gln Ile Leu
35          40          45

Thr Ala Leu Ala Val Ser Arg Val Gly Leu Leu Trp Val Leu Val Leu
50          55          60

Asn Trp Tyr Ala Thr Glu Leu Asn Pro Ala Phe Asn Ser Ile Glu Val
65          70          75          80

Arg Ile Thr Ala Tyr Asn Val Trp Ala Val Ile Asn His Phe Ser Asn
85          90          95

Trp Leu Ala Thr Ser Leu Ser Ile Phe Tyr Leu Leu Lys Ile Ala Asn
100         105         110

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Phe Ser Asn Leu Ile Phe Leu His Leu Lys Arg Arg Val Lys Ser Val
 115 120 125
 Val Leu Val Ile Leu Leu Gly Pro Leu Leu Phe Leu Val Cys His Leu
 130 135 140
 Phe Val Ile Asn Met Asn Gln Ile Ile Trp Thr Lys Glu Tyr Glu Gly
 145 150 155 160
 Asn Met Thr Trp Lys Ile Lys Leu Arg Ser Ala Met Tyr Leu Ser Asn
 165 170 175
 Thr Thr Val Thr Ile Leu Ala Asn Leu Val Pro Phe Thr Leu Thr Leu
 180 185 190
 Ile Ser Phe Leu Leu Leu Ile Cys Ser Leu Cys Lys His Leu Lys Lys
 195 200 205
 Met Gln Leu His Gly Lys Gly Ser Gln Asp Pro Ser Met Lys Val His
 210 215 220
 Ile Lys Ala Leu Gln Thr Val Thr Ser Phe Leu Leu Ile Cys Ala Ile
 225 230 235 240
 Tyr Phe Leu Ser Ile Ile Met Ser Val Trp Ser Phe Glu Ser Leu Glu
 245 250 255
 Asn Lys Pro Val Phe Met Phe Cys Glu Ala Ile Ala Phe Ser Tyr Pro
 260 265 270
 Ser Thr His Pro Phe Ile Leu Ile Trp Gly Asn Lys Lys Leu Lys Gln
 275 280 285
 Thr Phe Leu Ser Val Leu Trp His Val Arg Tyr Trp Val Lys Gly Glu
 290 295 300
 Lys Pro Ser Ser Ser
 305

<210> 192

<211> 930

<212> DNA

<213> Homo sapiens

<400> 192

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atctcctcag ctgaccaaatt cctcactgct ctggtggtct ccagaattgg ttactctgg      180
gtcatattat tacattggta tgcaaattgtg tttaattcag ctttatatag ttcagaagta      240
ggagctgttg cttctaatat ctcagcaata atcaaccatt tcagcatctg gcttgctgct      300
agcctcagca tattttatatt gctcaagatt gccaatctct ccaaccttat ttttctccac      360

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ctaaagaaga gaattaggag tgttggtctg gtgatactgt tgggtccctt ggtatTTTTg	420
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aatgtgactt ggaagatcaa attgaggaat gcaatacacc tttcaaactt gactgtaagc	540
acactagcaa acctcatacc ctTcattctg accctaatat gTTTTctgct gTtaatctgt	600
tctctgcata aacatctcaa gaagatgcag ctccatggca aaggatctca agatctcagc	660
accaaggtcc acataaaagc tttgcaaact gtgatctcct tcctcatggt atatgccatt	720
tactttctgt atctaatacac attaacctgg aatctttgaa cacagcagaa caaacttgta	780
ttctgctttt gccaaactct tggaatcatg tatcttcat tccactcatt ctTctgatt	840
atgggaagca ggaaactaaa acagacgttt ctttcagttt tatgtcaggt cacatgctta	900
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<210> 193

<211> 885

<212> DNA

<213> Homo sapiens

<400> 193

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atctcatcag ctgaccaaTt ttctcactgc tctggTggTg tccagagttg gtttactctg	180
ggTcatatta ttacattggT atgcaactgt gTTtaatttg gcttcacata gattagaagt	240
aagaatTTTT ggttctaattg tctcagcaat aaccaagcat ttcagcatct gggTgttact	300
agcctcagca tatTTcattt gctcaagact gccaatTTct ccaaccttat ttttctccac	360
ctaaagaaaa ggattaagaa tgttggtttg gtgatgctgt tggggccctt ggtatTTTTc	420
atTTgtaatc ttgctctgat aaccacgggt gagagtgtgt ggacaaaaga atatgaagga	480
aatttgtctt ggatgatcaa attgaggaat gcaatacagc tttcaaactt gactgtaacc	540
atgccagcaa acgtcacacc ctgcactctg acactaatat cTTTTctgct gTtaatctat	600
tctccatgta aacatgtcaa gaagatgcag ctccatggca aaggatctca acatctcagc	660
accaaggtgc acataaaagc tttgcaaact gtgatctcct tccttatggt atttgccatt	720
tactttctgt gtctaatacac atcaacttgT aatcctagga ctcagcagag caaacttgta	780
ttctgctttt accaaactct tggattcatg tatcttttTg tccactcatt catctgact	840
atgggaagta ggaagccaaa acagaccttt ctttcagctt tgtga	885

<210> 194
 <211> 912
 <212> DNA
 <213> Mus musculus

<400> 194
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 gggactacag tgaatggatt ccttatcatt gtgaactgct atgacttggt caagagccga 120
 acgttcctga tcctgcagac cctcttgatg tgcacagggc tgtccagact cggctctgcag 180
 ataatgctca tgacccaaag cttctttctct gtgttctttc cataactctta tgaggaaaat 240
 atttatagtt cagatataat gttcgtctgg atgttcttca gctcgattgg cctctgggtt 300
 gccacatgtc tctctgtctt ttactgcctc aagatttcag gcttcaactcc accctgggtt 360
 ctttggtctga aattcagaat ttcaaagctc atattttggc tgcttctggg cagcttgctg 420
 gcctctctgg gcaactgcaac tgtgtgcac gaggtagggt tccctttaat tgaggatggc 480
 tatgtcctga gaaacgcagg actaaatgat agtaatgcc aagtagtgag aaataatgac 540
 ttgctcctca tcaacctgat cctcctgctt cccctgtctg tgtttgtgat gtgcacctct 600
 atgttatttg tttctcttta caagcacatg cactggatgc aaagcgaatc tcacaagctg 660
 tcaagtgcc gaaccgaagc tcatataaat gcattaaaga cagtgacaac attcttttgt 720
 ttctttgttt cttactttgc tgccttcatg gcaaatatga catttagaat tccatacaga 780
 agtcatcagt tcttcgtggg gaaggaaatc atggcagcat atcccgcgg ccactctgtc 840
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 aaggaagagt ga 912

<210> 195
 <211> 303
 <212> PRT
 <213> Mus musculus

<400> 195
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 20 25 30
 Cys Tyr Asp Leu Phe Lys Ser Arg Thr Phe Leu Ile Leu Gln Thr Leu
 35 40 45
 Leu Met Cys Thr Gly Leu Ser Arg Leu Gly Leu Gln Ile Met Leu Met
 50 55 60

Thr Gln Ser Phe Phe Ser Val Phe Phe Pro Tyr Ser Tyr Glu Glu Asn
 65 70 75 80
 Ile Tyr Ser Ser Asp Ile Met Phe Val Trp Met Phe Phe Ser Ser Ile
 85 90 95
 Gly Leu Trp Phe Ala Thr Cys Leu Ser Val Phe Tyr Cys Leu Lys Ile
 100 105 110
 Ser Gly Phe Thr Pro Pro Trp Phe Leu Trp Leu Lys Phe Arg Ile Ser
 115 120 125
 Lys Leu Ile Phe Trp Leu Leu Leu Gly Ser Leu Leu Ala Ser Leu Gly
 130 135 140
 Thr Ala Thr Val Cys Ile Glu Val Gly Phe Pro Leu Ile Glu Asp Gly
 145 150 155 160
 Tyr Val Leu Arg Asn Ala Gly Leu Asn Asp Ser Asn Ala Lys Leu Val
 165 170 175
 Arg Asn Asn Asp Leu Leu Leu Ile Asn Leu Ile Leu Leu Leu Pro Leu
 180 185 190
 Ser Val Phe Val Met Cys Thr Ser Met Leu Phe Val Ser Leu Tyr Lys
 195 200 205
 His Met His Trp Met Gln Ser Glu Ser His Leu Lys Ser Ser Ala Arg
 210 215 220
 Thr Glu Ala His Ile Asn Ala Leu Lys Thr Val Thr Thr Phe Phe Cys
 225 230 235 240
 Phe Phe Val Ser Tyr Phe Ala Ala Phe Met Ala Asn Met Thr Phe Arg
 245 250 255
 Ile Pro Tyr Arg Ser His Gln Phe Phe Val Val Lys Glu Ile Met Ala
 260 265 270
 Ala Tyr Pro Ala Gly His Ser Val Ile Ile Val Leu Ser Asn Ser Lys
 275 280 285
 Phe Lys Asp Leu Phe Arg Arg Met Ile Cys Leu Gln Lys Glu Glu
 290 295 300

<210> 196

<211> 858

<212> PRT

<213> Mus musculus

<400> 196

Met Pro Gly Leu Ala Ile Leu Gly Leu Ser Leu Ala Ala Phe Leu Glu
 1 5 10 15
 Leu Gly Met Gly Ser Ser Leu Cys Leu Ser Gln Gln Phe Lys Ala Gln
 20 25 30

Gly	Asp	Tyr	Ile	Leu	Gly	Gly	Leu	Phe	Pro	Leu	Gly	Thr	Thr	Glu	Glu
	35						40					45			
Ala	Thr	Leu	Asn	Gln	Arg	Thr	Gln	Pro	Asn	Gly	Ile	Leu	Cys	Thr	Arg
	50					55					60				
Phe	Ser	Pro	Leu	Gly	Leu	Phe	Leu	Ala	Met	Ala	Met	Lys	Met	Ala	Val
65					70					75					80
Glu	Glu	Ile	Asn	Asn	Gly	Ser	Ala	Leu	Leu	Pro	Gly	Leu	Arg	Leu	Gly
				85					90					95	
Tyr	Asp	Leu	Phe	Asp	Thr	Cys	Ser	Glu	Pro	Val	Val	Thr	Met	Lys	Pro
			100					105					110		
Ser	Leu	Met	Phe	Met	Ala	Lys	Val	Gly	Ser	Gln	Ser	Ile	Ala	Ala	Tyr
		115					120					125			
Cys	Asn	Tyr	Thr	Gln	Tyr	Gln	Pro	Arg	Val	Leu	Ala	Val	Ile	Gly	Pro
	130					135					140				
His	Ser	Ser	Glu	Leu	Ala	Leu	Ile	Thr	Gly	Lys	Phe	Phe	Ser	Phe	Phe
145					150					155					160
Leu	Met	Pro	Gln	Val	Ser	Tyr	Ser	Ala	Ser	Met	Asp	Arg	Leu	Ser	Asp
				165					170					175	
Arg	Glu	Thr	Phe	Pro	Ser	Phe	Phe	Arg	Thr	Val	Pro	Ser	Asp	Arg	Val
			180					185					190		
Gln	Leu	Gln	Ala	Val	Val	Thr	Leu	Leu	Gln	Asn	Phe	Ser	Trp	Asn	Trp
		195					200					205			
Val	Ala	Ala	Leu	Gly	Ser	Asp	Asp	Asp	Tyr	Gly	Arg	Glu	Gly	Leu	Ser
	210					215					220				
Ile	Phe	Ser	Gly	Leu	Ala	Asn	Ser	Arg	Gly	Ile	Cys	Ile	Ala	His	Glu
225					230					235					240
Gly	Leu	Val	Pro	Gln	His	Asp	Thr	Ser	Gly	Gln	Gln	Leu	Gly	Lys	Val
				245					250					255	
Val	Asp	Val	Leu	Arg	Gln	Val	Asn	Gln	Ser	Lys	Val	Gln	Val	Val	Val
			260					265					270		
Leu	Phe	Ala	Ser	Ala	Arg	Ala	Val	Tyr	Ser	Leu	Phe	Ser	Tyr	Ser	Ile
		275					280					285			
Leu	His	Asp	Leu	Ser	Pro	Lys	Val	Trp	Val	Ala	Ser	Glu	Ser	Trp	Leu
	290					295					300				
Thr	Ser	Asp	Leu	Val	Met	Thr	Leu	Pro	Asn	Ile	Ala	Arg	Val	Gly	Thr
305					310					315					320
Val	Leu	Gly	Phe	Leu	Gln	Arg	Gly	Ala	Leu	Leu	Pro	Glu	Phe	Ser	His
				325					330					335	

Tyr	Val	Glu	Thr	Arg	Leu	Ala	Leu	Ala	Ala	Asp	Pro	Thr	Phe	Cys	Ala		
			340					345					350				
Ser	Leu	Lys	Ala	Glu	Leu	Asp	Leu	Glu	Glu	Arg	Val	Met	Gly	Pro	Arg		
		355					360					365					
Cys	Ser	Gln	Cys	Asp	Tyr	Ile	Met	Leu	Gln	Asn	Leu	Ser	Ser	Gly	Leu		
		370				375					380						
Met	Gln	Asn	Leu	Ser	Ala	Gly	Gln	Leu	His	His	Gln	Ile	Phe	Ala	Thr		
385					390					395					400		
Tyr	Ala	Ala	Val	Tyr	Ser	Val	Ala	Gln	Ala	Leu	His	Asn	Thr	Leu	Gln		
				405					410						415		
Cys	Asn	Val	Ser	His	Cys	His	Thr	Ser	Glu	Pro	Val	Gln	Pro	Trp	Gln		
			420					425					430				
Leu	Leu	Glu	Asn	Met	Tyr	Asn	Met	Ser	Phe	Arg	Ala	Arg	Asp	Leu	Thr		
		435					440					445					
Leu	Gln	Phe	Asp	Ala	Lys	Gly	Ser	Val	Asp	Met	Glu	Tyr	Asp	Leu	Lys		
	450					455					460						
Met	Trp	Val	Trp	Gln	Ser	Pro	Thr	Pro	Val	Leu	His	Thr	Val	Gly	Thr		
465					470					475					480		
Phe	Asn	Gly	Thr	Leu	Gln	Leu	Gln	His	Ser	Lys	Met	Tyr	Trp	Pro	Gly		
			485						490					495			
Asn	Gln	Val	Pro	Val	Ser	Gln	Cys	Ser	Arg	Gln	Cys	Lys	Asp	Gly	Gln		
			500					505					510				
Val	Arg	Arg	Val	Lys	Gly	Phe	His	Ser	Cys	Cys	Tyr	Asp	Cys	Val	Asp		
		515					520					525					
Cys	Lys	Ala	Gly	Ser	Tyr	Arg	Lys	His	Pro	Asp	Asp	Phe	Thr	Cys	Thr		
	530					535					540						
Pro	Cys	Gly	Lys	Asp	Gln	Trp	Ser	Pro	Glu	Lys	Ser	Thr	Thr	Cys	Leu		
545					550					555					560		
Pro	Arg	Arg	Pro	Lys	Phe	Leu	Ala	Trp	Gly	Glu	Pro	Ala	Val	Leu	Ser		
				565					570					575			
Leu	Leu	Leu	Leu	Leu	Cys	Leu	Val	Leu	Gly	Leu	Thr	Leu	Ala	Ala	Leu		
			580					585					590				
Gly	Leu	Phe	Val	His	Tyr	Trp	Asp	Ser	Pro	Leu	Val	Gln	Ala	Ser	Gly		
		595					600					605					
Gly	Ser	Leu	Phe	Cys	Phe	Gly	Leu	Ile	Cys	Leu	Gly	Leu	Phe	Cys	Leu		
	610					615					620						
Ser	Val	Leu	Leu	Phe	Pro	Gly	Arg	Pro	Arg	Ser	Ala	Ser	Cys	Leu	Ala		
625					630					635					640		

Gln Gln Pro Met Ala His Leu Pro Leu Thr Gly Cys Leu Ser Thr Leu
 645 650 655
 Phe Leu Gln Ala Ala Glu Ile Phe Val Glu Ser Glu Leu Pro Leu Ser
 660 665 670
 Trp Ala Asn Trp Leu Cys Ser Tyr Leu Arg Gly Pro Trp Ala Trp Leu
 675 680 685
 Val Val Leu Leu Ala Thr Leu Val Glu Ala Ala Leu Cys Ala Trp Tyr
 690 695 700
 Leu Met Ala Phe Pro Pro Glu Val Val Thr Asp Trp Gln Val Leu Pro
 705 710 715 720
 Thr Glu Val Leu Glu His Cys Arg Met Arg Ser Trp Val Ser Leu Gly
 725 730 735
 Leu Val His Ile Thr Asn Ala Val Leu Ala Phe Leu Cys Phe Leu Gly
 740 745 750
 Thr Phe Leu Val Gln Ser Gln Pro Gly Arg Tyr Asn Arg Ala Arg Gly
 755 760 765
 Leu Thr Phe Ala Met Leu Ala Tyr Phe Ile Ile Trp Val Ser Phe Val
 770 775 780
 Pro Leu Leu Ala Asn Val Gln Val Ala Tyr Gln Pro Ala Val Gln Met
 785 790 795 800
 Gly Ala Ile Leu Phe Cys Ala Leu Gly Ile Leu Ala Thr Phe His Leu
 805 810 815
 Pro Lys Cys Tyr Val Leu Leu Trp Leu Pro Glu Leu Asn Thr Gln Glu
 820 825 830
 Phe Phe Leu Gly Arg Ser Pro Lys Glu Ala Ser Asp Gly Asn Ser Gly
 835 840 845
 Ser Ser Glu Ala Thr Arg Gly His Ser Glu
 850 855

<210> 197

<211> 841

<212> PRT

<213> Homo sapiens

<400> 197

Met Leu Leu Cys Thr Ala Arg Leu Val Gly Leu Gln Leu Leu Ile Ser
 1 5 10 15

Cys Cys Trp Ala Phe Ala Cys His Ser Thr Glu Ser Ser Pro Asp Phe
 20 25 30

Thr Leu Pro Gly Asp Tyr Leu Leu Ala Gly Leu Phe Pro Leu His Ser
 35 40 45

Gly	Cys	Leu	Gln	Val	Arg	His	Arg	Pro	Glu	Val	Thr	Leu	Cys	Asp	Arg	50	55	60
Ser	Cys	Ser	Phe	Asn	Glu	His	Gly	Tyr	His	Leu	Phe	Gln	Ala	Met	Arg	65	70	75
Leu	Gly	Val	Glu	Glu	Ile	Asn	Asn	Ser	Thr	Ala	Leu	Leu	Pro	Asn	Ile	85	90	95
Thr	Leu	Gly	Tyr	Gln	Leu	Tyr	Asp	Val	Cys	Ser	Asp	Ser	Ala	Asn	Val	100	105	110
Tyr	Ala	Thr	Leu	Arg	Val	Leu	Ser	Leu	Pro	Gly	Gln	His	His	Ile	Glu	115	120	125
Leu	Gln	Gly	Asp	Leu	Leu	His	Tyr	Ser	Pro	Thr	Val	Leu	Ala	Val	Ile	130	135	140
Gly	Pro	Asp	Ser	Thr	Asn	Arg	Ala	Ala	Thr	Thr	Ala	Ala	Leu	Leu	Ser	145	150	155
Pro	Phe	Leu	Val	Pro	Met	Ile	Ser	Tyr	Ala	Ala	Ser	Ser	Glu	Thr	Leu	165	170	175
Ser	Val	Lys	Arg	Gln	Tyr	Pro	Ser	Phe	Leu	Arg	Thr	Ile	Pro	Asn	Asp	180	185	190
Lys	Tyr	Gln	Val	Glu	Thr	Met	Val	Leu	Leu	Leu	Gln	Lys	Phe	Gly	Trp	195	200	205
Thr	Trp	Ile	Ser	Leu	Val	Gly	Ser	Ser	Asp	Asp	Tyr	Gly	Gln	Leu	Gly	210	215	220
Val	Gln	Ala	Leu	Glu	Asn	Gln	Ala	Thr	Gly	Gln	Gly	Ile	Cys	Ile	Ala	225	230	235
Phe	Lys	Asp	Ile	Met	Pro	Phe	Ser	Ala	Gln	Val	Gly	Asp	Glu	Arg	Met	245	250	255
Gln	Cys	Leu	Met	Arg	His	Leu	Ala	Gln	Ala	Gly	Ala	Thr	Val	Val	Val	260	265	270
Val	Phe	Ser	Ser	Arg	Gln	Leu	Ala	Arg	Val	Phe	Phe	Glu	Ser	Val	Val	275	280	285
Leu	Thr	Asn	Leu	Thr	Gly	Lys	Val	Trp	Val	Ala	Ser	Glu	Ala	Trp	Ala	290	295	300
Leu	Ser	Arg	His	Ile	Thr	Gly	Val	Pro	Gly	Ile	Gln	Arg	Ile	Gly	Met	305	310	315
Val	Leu	Gly	Val	Ala	Ile	Gln	Lys	Arg	Ala	Val	Pro	Gly	Leu	Lys	Ala	325	330	335
Phe	Glu	Glu	Ala	Tyr	Ala	Arg	Ala	Asp	Lys	Lys	Ala	Pro	Arg	Pro	Cys	340	345	350

His	Lys	Gly	Ser	Trp	Cys	Ser	Ser	Asn	Gln	Leu	Cys	Arg	Glu	Cys	Gln
		355					360					365			
Ala	Phe	Met	Ala	His	Thr	Met	Pro	Lys	Leu	Lys	Ala	Phe	Ser	Met	Ser
		370					375					380			
Ser	Ala	Tyr	Asn	Ala	Tyr	Arg	Ala	Val	Tyr	Ala	Val	Ala	His	Gly	Leu
385					390					395					
His	Gln	Leu	Leu	Gly	Cys	Ala	Ser	Gly	Ala	Cys	Ser	Arg	Gly	Arg	Val
				405					410					415	
Tyr	Pro	Trp	Gln	Leu	Leu	Glu	Gln	Ile	His	Lys	Val	His	Phe	Leu	Leu
				420					425					430	
His	Lys	Asp	Thr	Val	Ala	Phe	Asn	Asp	Asn	Arg	Asp	Pro	Leu	Ser	Ser
		435					440					445			
Tyr	Asn	Ile	Ile	Ala	Trp	Asp	Trp	Asn	Gly	Pro	Lys	Trp	Thr	Phe	Thr
		450					455					460			
Val	Leu	Gly	Ser	Ser	Thr	Trp	Ser	Pro	Val	Gln	Leu	Asn	Ile	Asn	Glu
465					470					475					
Thr	Lys	Ile	Gln	Trp	His	Gly	Lys	Asp	Asn	Gln	Val	Pro	Lys	Ser	Val
				485					490					495	
Cys	Ser	Ser	Asp	Cys	Leu	Glu	Gly	His	Gln	Arg	Val	Val	Thr	Gly	Phe
				500					505					510	
His	His	Cys	Cys	Phe	Glu	Cys	Val	Pro	Cys	Gly	Ala	Gly	Thr	Phe	Leu
		515					520					525			
Asn	Lys	Ser	Asp	Leu	Tyr	Arg	Cys	Gln	Pro	Cys	Gly	Lys	Glu	Glu	Trp
		530					535					540			
Ala	Pro	Glu	Gly	Ser	Gln	Thr	Cys	Phe	Pro	Arg	Thr	Val	Val	Phe	Leu
545					550					555					
Ala	Leu	Arg	Glu	His	Thr	Ser	Trp	Val	Leu	Leu	Ala	Ala	Asn	Thr	Leu
				565					570					575	
Leu	Leu	Leu	Leu	Leu	Leu	Gly	Thr	Ala	Gly	Leu	Phe	Ala	Trp	His	Leu
				580					585					590	
Asp	Thr	Pro	Val	Val	Arg	Ser	Ala	Gly	Gly	Arg	Leu	Cys	Phe	Leu	Met
		595					600					605			
Leu	Gly	Ser	Leu	Ala	Ala	Gly	Ser	Gly	Ser	Leu	Tyr	Gly	Phe	Phe	Gly
		610					615					620			
Glu	Pro	Thr	Arg	Pro	Ala	Cys	Leu	Leu	Arg	Gln	Ala	Leu	Phe	Ala	Leu
625					630					635					
Gly	Phe	Thr	Ile	Phe	Leu	Ser	Cys	Leu	Thr	Val	Arg	Ser	Phe	Gln	Leu
				645					650					655	

Ile Ile Ile Phe Lys Phe Ser Thr Lys Val Pro Thr Phe Tyr His Ala
 660 665 670
 Trp Val Gln Asn His Gly Ala Gly Leu Phe Val Met Ile Ser Ser Ala
 675 680 685
 Ala Gln Leu Leu Ile Cys Leu Thr Trp Leu Val Val Trp Thr Pro Leu
 690 695 700
 Pro Ala Arg Glu Tyr Gln Arg Phe Pro His Leu Val Met Leu Glu Cys
 705 710 715 720
 Thr Glu Thr Asn Ser Leu Gly Phe Ile Leu Ala Phe Leu Tyr Asn Gly
 725 730 735
 Leu Leu Ser Ile Ser Ala Phe Ala Cys Ser Tyr Leu Gly Lys Asp Leu
 740 745 750
 Pro Glu Asn Tyr Asn Glu Ala Lys Cys Val Thr Phe Ser Leu Leu Phe
 755 760 765
 Asn Phe Val Ser Trp Ile Ala Phe Phe Thr Thr Ala Ser Val Tyr Asp
 770 775 780
 Gly Lys Tyr Leu Pro Ala Ala Asn Met Met Ala Gly Leu Ser Ser Leu
 785 790 795 800
 Ser Ser Gly Phe Gly Gly Tyr Phe Leu Pro Lys Cys Tyr Val Ile Leu
 805 810 815
 Cys Arg Pro Asp Leu Asn Ser Thr Glu His Phe Gln Ala Ser Ile Gln
 820 825 830
 Asp Tyr Thr Arg Arg Cys Gly Ser Thr
 835 840

<210> 198
 <211> 839
 <212> PRT
 <213> Homo sapiens

<400> 198
 Met Gly Pro Arg Ala Lys Thr Ile Cys Ser Leu Phe Phe Leu Leu Trp
 1 5 10 15
 Val Leu Ala Glu Pro Ala Glu Asn Ser Asp Phe Tyr Leu Pro Gly Asp
 20 25 30
 Tyr Leu Leu Gly Gly Leu Phe Ser Leu His Ala Asn Met Lys Gly Ile
 35 40 45
 Val His Leu Asn Phe Leu Gln Val Pro Met Cys Lys Glu Tyr Glu Val
 50 55 60
 Lys Val Ile Gly Tyr Asn Leu Met Gln Ala Met Arg Phe Ala Val Glu
 65 70 75 80

Glu	Ile	Asn	Asn	Asp	Ser	Ser	Leu	Leu	Pro	Gly	Val	Leu	Leu	Gly	Tyr		
				85					90					95			
Glu	Ile	Val	Asp	Val	Cys	Tyr	Ile	Ser	Asn	Asn	Val	Gln	Pro	Val	Leu		
			100					105					110				
Tyr	Phe	Leu	Ala	His	Glu	Asp	Asn	Leu	Leu	Pro	Ile	Gln	Glu	Asp	Tyr		
		115					120					125					
Ser	Asn	Tyr	Ile	Ser	Arg	Val	Val	Ala	Val	Ile	Gly	Pro	Asp	Asn	Ser		
	130					135					140						
Glu	Ser	Val	Met	Thr	Val	Ala	Asn	Phe	Leu	Ser	Leu	Phe	Leu	Leu	Pro		
145					150					155					160		
Gln	Ile	Thr	Tyr	Ser	Ala	Ile	Ser	Asp	Glu	Leu	Arg	Asp	Lys	Val	Arg		
				165					170					175			
Phe	Pro	Ala	Leu	Leu	Arg	Thr	Thr	Pro	Ser	Ala	Asp	His	His	Val	Glu		
			180					185					190				
Ala	Met	Val	Gln	Leu	Met	Leu	His	Phe	Arg	Trp	Asn	Trp	Ile	Ile	Val		
	195						200					205					
Leu	Val	Ser	Ser	Asp	Thr	Tyr	Gly	Arg	Asp	Asn	Gly	Gln	Leu	Leu	Gly		
	210					215					220						
Glu	Arg	Val	Ala	Arg	Arg	Asp	Ile	Cys	Ile	Ala	Phe	Gln	Glu	Thr	Leu		
225					230					235					240		
Pro	Thr	Leu	Gln	Pro	Asn	Gln	Asn	Met	Thr	Ser	Glu	Glu	Arg	Gln	Arg		
				245					250					255			
Leu	Val	Thr	Ile	Val	Asp	Lys	Leu	Gln	Gln	Ser	Thr	Ala	Arg	Val	Val		
			260					265					270				
Val	Val	Phe	Ser	Pro	Asp	Leu	Thr	Leu	Tyr	His	Phe	Phe	Asn	Glu	Val		
		275					280					285					
Leu	Arg	Gln	Asn	Phe	Thr	Gly	Ala	Val	Trp	Ile	Ala	Ser	Glu	Ser	Trp		
	290					295					300						
Ala	Ile	Asp	Pro	Val	Leu	His	Asn	Leu	Thr	Glu	Leu	Gly	His	Leu	Gly		
305					310					315					320		
Thr	Phe	Leu	Gly	Ile	Thr	Ile	Gln	Ser	Val	Pro	Ile	Pro	Gly	Phe	Ser		
				325					330					335			
Glu	Phe	Arg	Glu	Trp	Gly	Pro	Gln	Ala	Gly	Pro	Pro	Pro	Leu	Ser	Arg		
			340					345					350				
Thr	Ser	Gln	Ser	Tyr	Thr	Cys	Asn	Gln	Glu	Cys	Asp	Asn	Cys	Leu	Asn		
		355					360					365					
Ala	Thr	Leu	Ser	Phe	Asn	Thr	Ile	Leu	Arg	Leu	Ser	Gly	Glu	Arg	Val		
	370					375					380						

Val	Tyr	Ser	Val	Tyr	Ser	Ala	Val	Tyr	Ala	Val	Ala	His	Ala	Leu	His
385					390					395					400
Ser	Leu	Leu	Gly	Cys	Asp	Lys	Ser	Thr	Cys	Thr	Lys	Arg	Val	Val	Tyr
			405						410					415	
Pro	Trp	Gln	Leu	Leu	Glu	Glu	Ile	Trp	Lys	Val	Asn	Phe	Thr	Leu	Leu
		420						425					430		
Asp	His	Gln	Ile	Phe	Phe	Asp	Pro	Gln	Gly	Asp	Val	Ala	Leu	His	Leu
		435					440					445			
Glu	Ile	Val	Gln	Trp	Gln	Trp	Asp	Arg	Ser	Gln	Asn	Pro	Phe	Gln	Ser
	450					455					460				
Val	Ala	Ser	Tyr	Tyr	Pro	Leu	Gln	Arg	Gln	Leu	Lys	Asn	Ile	Gln	Asp
465					470					475					480
Ile	Ser	Trp	His	Thr	Val	Asn	Asn	Thr	Ile	Pro	Met	Ser	Met	Cys	Ser
			485						490					495	
Lys	Arg	Cys	Gln	Ser	Gly	Gln	Lys	Lys	Lys	Pro	Val	Gly	Ile	His	Val
			500					505					510		
Cys	Cys	Phe	Glu	Cys	Ile	Asp	Cys	Leu	Pro	Gly	Thr	Phe	Leu	Asn	His
		515					520					525			
Thr	Glu	Asp	Glu	Tyr	Glu	Cys	Gln	Ala	Cys	Pro	Asn	Asn	Glu	Trp	Ser
	530					535					540				
Tyr	Gln	Ser	Glu	Thr	Ser	Cys	Phe	Lys	Arg	Gln	Leu	Val	Phe	Leu	Glu
545					550					555					560
Trp	His	Glu	Ala	Pro	Thr	Ile	Ala	Val	Ala	Leu	Leu	Ala	Ala	Leu	Gly
				565					570					575	
Phe	Leu	Ser	Thr	Leu	Ala	Ile	Leu	Val	Ile	Phe	Trp	Arg	His	Phe	Gln
			580					585					590		
Thr	Pro	Ile	Val	Arg	Ser	Ala	Gly	Gly	Pro	Met	Cys	Phe	Leu	Met	Leu
		595					600					605			
Thr	Leu	Leu	Leu	Val	Ala	Tyr	Met	Val	Val	Pro	Val	Tyr	Val	Gly	Pro
	610					615					620				
Pro	Lys	Val	Ser	Thr	Cys	Leu	Cys	Arg	Gln	Ala	Leu	Phe	Pro	Leu	Cys
625					630					635					640
Phe	Thr	Ile	Cys	Ile	Ser	Cys	Ile	Ala	Val	Arg	Ser	Phe	Gln	Ile	Val
				645					650					655	
Cys	Ala	Phe	Lys	Met	Ala	Ser	Arg	Phe	Pro	Arg	Ala	Tyr	Ser	Tyr	Trp
			660					665					670		
Val	Arg	Tyr	Gln	Gly	Pro	Tyr	Val	Ser	Met	Ala	Phe	Ile	Thr	Val	Leu
		675					680					685			

Lys Met Val Ile Val Val Ile Gly Met Leu Ala Thr Gly Leu Ser Pro
 690 695 700
 Thr Thr Arg Thr Asp Pro Asp Asp Pro Lys Ile Thr Ile Val Ser Cys
 705 710 715 720
 Asn Pro Asn Tyr Arg Asn Ser Leu Leu Phe Asn Thr Ser Leu Asp Leu
 725 730 735
 Leu Leu Ser Val Val Gly Phe Ser Phe Ala Tyr Met Gly Lys Glu Leu
 740 745 750
 Pro Thr Asn Tyr Asn Glu Ala Lys Phe Ile Thr Leu Ser Met Thr Phe
 755 760 765
 Tyr Phe Thr Ser Ser Val Ser Leu Cys Thr Phe Met Ser Ala Tyr Ser
 770 775 780
 Gly Val Leu Val Thr Ile Val Asp Leu Leu Val Thr Val Leu Asn Leu
 785 790 795 800
 Leu Ala Ile Ser Leu Gly Tyr Phe Gly Pro Lys Cys Tyr Met Ile Leu
 805 810 815
 Phe Tyr Pro Glu Arg Asn Thr Pro Ala Tyr Phe Asn Ser Met Ile Gln
 820 825 830
 Gly Tyr Thr Met Arg Arg Asp
 835

<210> 199
 <211> 852
 <212> PRT
 <213> Homo sapiens

<400> 199
 Met Leu Gly Pro Ala Val Leu Gly Leu Ser Leu Trp Ala Leu Leu His
 1 5 10 15
 Pro Gly Thr Gly Ala Pro Leu Cys Leu Ser Gln Gln Leu Arg Met Lys
 20 25 30
 Gly Asp Tyr Val Leu Gly Gly Leu Phe Pro Leu Gly Glu Ala Glu Glu
 35 40 45
 Ala Gly Leu Arg Ser Arg Thr Arg Pro Ser Ser Pro Val Cys Thr Arg
 50 55 60
 Phe Ser Ser Asn Gly Leu Leu Trp Ala Leu Ala Met Lys Met Ala Val
 65 70 75 80
 Glu Glu Ile Asn Asn Lys Ser Asp Leu Leu Pro Gly Leu Arg Leu Gly
 85 90 95
 Tyr Asp Leu Phe Asp Thr Cys Ser Glu Pro Val Val Ala Met Lys Pro
 100 105 110

Ser	Leu	Met	Phe	Leu	Ala	Lys	Ala	Gly	Ser	Arg	Asp	Ile	Ala	Ala	Tyr	115	120	125	
Cys	Asn	Tyr	Thr	Gln	Tyr	Gln	Pro	Arg	Val	Leu	Ala	Val	Ile	Gly	Pro	130	135	140	
His	Ser	Ser	Glu	Leu	Ala	Met	Val	Thr	Gly	Lys	Phe	Phe	Ser	Phe	Phe	145	150	155	160
Leu	Met	Pro	Gln	Val	Ser	Tyr	Gly	Ala	Ser	Met	Glu	Leu	Leu	Ser	Ala	165	170	175	
Arg	Glu	Thr	Phe	Pro	Ser	Phe	Phe	Arg	Thr	Val	Pro	Ser	Asp	Arg	Val	180	185	190	
Gln	Leu	Thr	Ala	Ala	Ala	Glu	Leu	Leu	Gln	Glu	Phe	Gly	Trp	Asn	Trp	195	200	205	
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caacaaccaa	tggtctcacct	ccctctcaca	ggctgcctga	gcacactctt	cctgcaagca	1980
gccgagatct	ttgtggagtc	tgagctgcca	ctgagttggg	caaactggct	ctgcagctac	2040
cttcggggcc	cctgggcttg	gctggtggta	ctgctggcca	ctcttggtga	ggctgcacta	2100
tgtgcctggt	acttgatggc	tttccctcca	gaggtggtga	cagattggca	ggtgctgccc	2160
acggaggtac	tggaacactg	ccgcatgcgt	tcctgggtca	gcctgggctt	ggtgcacatc	2220
accaatgcag	tgttagcttt	cctctgcttt	ctgggcactt	tcctggtaca	gagccagcct	2280
ggtcgctata	accgtgccc	tggcctcacc	ttcgccatgc	tagcttat	catcatctgg	2340
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ggtgctatct	tattctgtgc	cctgggcac	ctggccacct	tccacctgcc	caa	2460
gtacttctgt	ggctgccaga	gctcaacacc	caggagtctt	tcctgggaag	gagccccaag	2520
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<210> 204

<211> 137

<212> PRT

<213> Fugu rubripes

<400> 204

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Pro Ser Pro Phe Arg Asp Ile Val Ser Tyr Pro Asp Lys Ile Ile Leu
1          5          10          15

Gly Cys Phe Met Asn Leu Lys Thr Ser Ser Val Ser Phe Val Leu Leu
          20          25          30

Leu Leu Leu Cys Leu Leu Cys Phe Ile Phe Ser Tyr Met Gly Lys Asp
          35          40          45

Leu Pro Lys Asn Tyr Asn Glu Ala Lys Ala Ile Thr Phe Cys Leu Leu
          50          55          60

Leu Leu Ile Leu Thr Trp Ile Ile Phe Thr Thr Ala Ser Leu Leu Tyr
65          70          75          80

Gln Gly Lys Tyr Ile His Ser Leu Asn Ala Leu Ala Val Leu Ser Ser
          85          90          95

Ile Tyr Ser Phe Leu Leu Trp Tyr Phe Leu Pro Lys Cys Tyr Ile Ile
          100          105          110

Ile Phe Gln Pro Gln Lys Asn Thr Gln Lys Tyr Phe Gln Gly Leu Ile
          115          120          125

Gln Asp Tyr Thr Lys Thr Ile Ser Gln
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<212> PRT

<213> Tetraodon nigroviridis

<220>

<221> MOD_RES

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<223> Variable amino acid

<400> 205

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Phe Ala Val Asn Tyr Asn Thr Pro Val Val Arg Ser Ala Gly Gly Pro
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Met Cys Phe Leu Ile Leu Gly Cys Leu Ser Leu Cys Ser Ile Ser Val
          20          25          30

Phe Phe Tyr Phe Glu Arg Pro Thr Glu Ala Phe Cys Ile Leu Arg Phe
          35          40          45

Met Pro Phe Leu Leu Phe Tyr Ala Val Cys Leu Ala Cys Phe Ala Val
          50          55          60

Arg Ser Phe Gln Ile Val Ile Ile Phe Lys Ile Ala Ala Lys Phe Pro
65          70          75          80

Arg Val His Ser Trp Trp Met Lys Tyr His Gly Gln Trp Leu Val Ile
          85          90          95

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Ser Met Thr Phe Val Leu Gln Ala Val Val Ile Val Ile Gly Phe Ser
 100 105 110
 Ser Asn Pro Pro Leu Pro Tyr Xaa Xaa Phe Val Ser Tyr Pro Asp Lys
 115 120 125
 Ile Ile Leu Gly Cys Asp Val Asn Leu Asn Met Ala Ser Thr Ser Phe
 130 135 140
 Phe Leu Leu Leu Leu Leu Cys Ile Leu Cys Phe Thr Phe Ser Tyr Met
 145 150 155 160
 Gly Lys Asp Leu Pro Lys Asn Tyr Asn Glu Ala Lys Ala Ile Thr Phe
 165 170 175
 Cys Leu Leu Leu Leu Ile Leu Thr Trp Ile Ile Phe Ala Thr Ala Phe
 180 185 190
 Met Leu Tyr His Gly Lys Tyr Ile His Thr Leu Asn Ala Leu Ala Val
 195 200 205
 Leu Ser Ser Ala Tyr Cys Phe Leu Leu Trp Tyr Phe Leu Pro Lys Cys
 210 215 220
 Tyr Ile Ile Ile Phe Gln Pro His Lys Asn Thr Gln Lys Tyr Phe Gln
 225 230 235 240
 Leu Ser

<210> 206
 <211> 165
 <212> PRT
 <213> Fugu rubripes

<400> 206
 Lys Lys Gln Gly Pro Glu Val Asp Ile Phe Ile Val Ser Val Thr Ile
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 Leu Cys Ile Ser Val Leu Gly Val Ala Val Gly Pro Pro Glu Pro Ser
 20 25 30
 Gln Asp Leu Asp Phe Tyr Met Asp Ser Ile Val Leu Glu Cys Ser Asn
 35 40 45
 Thr Leu Ser Pro Gly Ser Phe Ile Glu Leu Cys Tyr Val Cys Val Leu
 50 55 60
 Ser Val Leu Cys Phe Phe Phe Ser Tyr Met Gly Lys Asp Leu Pro Ala
 65 70 75 80
 Asn Tyr Asn Glu Ala Lys Cys Val Thr Phe Ser Leu Met Val Tyr Met
 85 90 95
 Ile Ser Trp Ile Ser Phe Phe Thr Val Tyr Leu Ile Ser Arg Gly Pro
 100 105 110

Phe Thr Val Ala Ala Tyr Val Cys Ala Thr Leu Val Ser Val Leu Ala
 115 120 125

Phe Phe Gly Gly Tyr Phe Leu Pro Lys Ile Tyr Ile Ile Val Leu Lys
 130 135 140

Pro Gln Met Asn Thr Thr Ala His Phe Gln Asn Cys Ile Gln Met Tyr
 145 150 155 160

Thr Met Ser Lys Gln
 165

<210> 207

<211> 236

<212> PRT

<213> Tetraodon nigroviridis

<220>

<221> MOD_RES

<222> (8)..(8)

<223> Variable amino acid

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<223> Variable amino acid

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<222> (136)..(136)

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 20 25 30
 Cys Leu Leu Met Thr Ser Ser Ser Ala Val Ile Leu Leu Leu Asn Ile
 35 40 45
 Asn Thr Pro Val Ala Lys Ser Ala Gly Gly Xaa Thr Cys Xaa Leu Lys
 50 55 60
 Leu Ala Ala Leu Thr Ala Ala Ala Met Ser Ser Xaa Cys His Phe Gly
 65 70 75 80
 Gln Pro Ser Pro Leu Ala Ser Lys Leu Lys Gln Pro Gln Phe Thr Phe
 85 90 95
 Ser Phe Thr Val Cys Leu Ala Cys Asn Arg Cys Ala Leu Ala Thr Gly
 100 105 110
 His Leu His Phe Xaa Ile Arg Val Ala Leu Pro Pro Ala Tyr Asn Xaa
 115 120 125
 Trp Ala Lys Asn His Gly Pro Xaa Ala Thr Ile Phe Ile Ala Ser Ala
 130 135 140
 Ala Ile Leu Cys Val Leu Cys Leu Arg Val Ala Val Gly Pro Pro Gln
 145 150 155 160
 Pro Ser Gln Asx Leu Asx Phe Xaa Thr Asn Ser Ile Xaa Leu Xaa Xaa
 165 170 175

Ser Asn Thr Leu Ser Pro Gly Ser Phe Val Glu Leu Cys Asn Val Ser
 180 185 190

Leu Leu Ser Ala Val Cys Phe Val Phe Ser Xaa Met Gly Lys Asx Leu
 195 200 205

Pro Ala Asn Tyr Asn Glu Ala Lys Cys Val Thr Phe Ser Leu Met Val
 210 215 220

Asn Xaa Ile Ser Trp Ile Ser Phe Phe Thr Val Tyr
 225 230 235

<210> 208
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 208
 Phe Lys Lys Ser Phe Lys Leu
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<210> 209
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 209
 Arg Arg Leu Ile Glu Asp Ala Glu Tyr Ala Ala Arg Gly
 1 5 10

<210> 210
 <211> 11
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic consensus
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<400> 210
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